

```
Db 597 LAMGII-ATIEVMATFIRYNDPIVRASGRELSTVLLTGIFLCY--ITF-L---MIA- 648
OY 487 LTLIGMNASAFLEPN-IKNRNOKLIKSSPYMNNLITLIGMLSTASIFLEGDSFVSE 545
Db 649 KPDVAVCSFRFVFLGNCISYALITKTRIRYIFEOGKRSYAPRLISPTSLAITS 708
OY 546 KTFEFLCTVRMILTVGTAFGAMFAKTWRVHAIFKNVKM-K-KIIDQQLVTVGG 602
Db 709 LISVOLLGVEI-WEGVDPPNIIID-YD-EKTMNPEQA-RGVLR-CDITDQI-ICSL-G 761
OY 603 MLIDIL-CILICQAVDPLRTRVYSMEPPDAGRDISIRPLEHCENTHMTIWLGIYA 661
Db 762 YSILMV-TC-TVYAIKTRGVENFNEAKPIGFTMYTCIWLAFIPFGTAQSAEKLY 819
OY 662 YKGLMLGCGFLAMETRVNSIPA-LNDSKYIGMSVYVNGIMCIIGAASVFLTRDQPNVOF 720
Db 820 IOTTTLTSMNLASVALGMLYMPKVIYIIIFPELVOKRRSF 863
OY 721 C-IVALVI-I-FCSITLCLVFPKLTITLTPDPAATONRRPOF 761
```

RESULT 15

```
ID R72098 standard; Protein; 922 AA.
AC R72098;
DT 26-SEP-1995 (first entry)
DE Human mGluR7b.
KW Human metabotropic glutamate receptor subtype 4; mGluR7; mGluR7;
KM signal transducer.
OS Homo sapiens.
PN M09508627-A.
PD 30-MAR-1995;
PF 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016553.
PA (CIBA ) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetzner I;
DR WPI: 95-139586/18.
DR N-PSDB; 089348.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PT cpts. which modulate signal transduction activity
PS Claim 7; Page 95-99; 110pp; English.
CC Human metabotropic glutamate receptor subtype 7 (mGluR7) cDNA
CC clones were isolated from fetal brain and hippocampus cDNA libraries
CC using a rat mGluR4 probe, and the 5' region missing from these
CC clones was generated by PCR from brain cDNA. Sequence comparison of
CC fetal brain and hippocampus clones indicated the existence of 2
CC subtypes of mGluR7, mGluR7a (given in R72097) and mGluR7b
CC (R72098). Full-length cDNA clones (089347-48) encoding these
CC proteins were expressed in mammalian cells.
SQ Sequence 922 AA;
```

Query Match 3.1%; Score 214; DB 1; Length 922;

Best Local Similarity 22.9%; Pred. No. 3.67e-06;

Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

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Db 597 LAMGII-ATIEVMATFIRYNDPIVRASGRELSTVLLTGIFLCY--ITF-L---MIA- 648
OY 487 LTLIGMNASAFLEPN-IKNRNOKLIKSSPYMNNLITLIGMLSTASIFLEGDSFVSE 545
Db 649 KPDVAVCSFRFVFLGNCISYALITKTRIRYIFEOGKRSYAPRLISPTSLAITS 708
OY 546 KTFEFLCTVRMILTVGTAFGAMFAKTWRVHAIFKNVKM-K-KIIDQQLVTVGG 602
Db 709 LISVOLLGVEI-WEGVDPPNIIID-YD-EKTMNPEQA-RGVLR-CDITDQI-ICSL-G 761
OY 603 MLIDIL-CILICQAVDPLRTRVYSMEPPDAGRDISIRPLEHCENTHMTIWLGIYA 661
Db 762 YSILMV-TC-TVYAIKTRGVENFNEAKPIGFTMYTCIWLAFIPFGTAQSAEKLY 819
OY 662 YKGLMLGCGFLAMETRVNSIPA-LNDSKYIGMSVYVNGIMCIIGAASVFLTRDQPNVOF 720
Db 820 IOTTTLTSMNLASVALGMLYMPKVIYIIIFPELVOKRRSF 863
```

```
OY 721 C-IVALVI-I-FCSITLCLVFPKLTITLTPDPAATONRRPOF 761
```

Search completed: Wed Mar 15 21:55:10 2000
Job time : 353 secs.


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Db 588 AVLPLEFLAVG-IAATLFVITFVRNDPIVKSAGRELSYVLAGIFLCYATTEL--M- 643
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 482 SLTISA-LTILGIMASAFLEFN-IKNRNOKLIKMSPPYNNLIIIGMLSYASIFLEGLD 539
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 644 ----IAEPDGLT-CSLRRIPLGSGMSIYVALLTKNRIYRIPEQGRKRSVSAPEFSPASQ 699
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 540 GSFVSEKTEFTLCYVWTWLTWGYTAFGAMFAKTWRHAIRKNV--MKR-KIIRDOKL 596
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 700 LAITFSLISLOI-LGICVWFVVDPSHSYVD-FODORTLDP--FA-RGYLK-CDISDSL- 753
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 597 LVTVGMLLIDLCILIC-WQAVDPLRRTYERYSMEPDPAGRDISIRPLEHCENHTMTW 655
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 754 ICLL-GYSMLLV-TC-TVYAIKTRGVPEFTEANRPIGFTMTTCIVWLAFIPFEGTSQ 810
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 656 LGIVYAKKGLMFCGFLAMETRNVSIP-ALNDSKYIGMSYVNGIMCIIIGAASFRTD 714
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 811 SMDKLIYOTITLVYSLSASVSLGMLYMPKYIILFHDEQVPRK 857
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 715 QPNVQFC-IVALVI-I-FCSTITLCLVFPVKLITLTNPDAATONRR 758
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
RESULT 10
ID R72092 standard; Protein: 912 AA.
AC R72092;
DT 26-SEP-1995 (first entry)
DE Human mglur4.
KW Human metabotropic glutamate receptor subtype 4; mglur4; hmglur4;
KM signal transducer.
OS Homo sapiens.
PN MO9508627-A.
PD 30-MAR-1995.
PE 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016553.
PA (CIBA ) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetzner I;
PI WPI; 95-139596/18.
DR N-PSDB; Q89342.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PS Clads, which modulate signal transduction activity
PS Claim 2; Page 44-48; 110pp; English.
CC Human metabotropic glutamate receptor subtype 4 (hmglur4) cDNA
CC clones were isolated from a cerebellum cDNA library using a rat
CC mglur4 probe. Clone cmr20 lacked the 5' end of the hmglur4 gene.
CC PCR using human genomic or brain cDNA as template was used to
CC obtain a complete gene sequence (given in Q89342) encoding hmglur4
CC (R72092). Recombinant hmglur4 was produced in mammalian cells.
SQ Sequence 912 AA;
```

```
Query Match 3.3%; Score 228; DB 1; Length 912;
Best Local Similarity 21.6%; Pred. No. 3.51e-07;
Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;
```

```
Db 588 AVLPLEFLAVG-IAATLFVITFVRNDPIVKSAGRELSYVLAGIFLCYATTEL--M- 643
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 482 SLTISA-LTILGIMASAFLEFN-IKNRNOKLIKMSPPYNNLIIIGMLSYASIFLEGLD 539
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 644 ----IAEPDGLT-CSLRRIPLGSGMSIYVALLTKNRIYRIPEQGRKRSVSAPEFSPASQ 699
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 540 GSFVSEKTEFTLCYVWTWLTWGYTAFGAMFAKTWRHAIRKNV--MKR-KIIRDOKL 596
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 700 LAITFSLISLOI-LGICVWFVVDPSHSYVD-FODORTLDP--FA-RGYLK-CDISDSL- 753
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 597 LVTVGMLLIDLCILIC-WQAVDPLRRTYERYSMEPDPAGRDISIRPLEHCENHTMTW 655
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 754 ICLL-GYSMLLV-TC-TVYAIKTRGVPEFTEANRPIGFTMTTCIVWLAFIPFEGTSQ 810
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 656 LGIVYAKKGLMFCGFLAMETRNVSIP-ALNDSKYIGMSYVNGIMCIIIGAASFRTD 714
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 811 SAKKIYIQTTLTVSVLSASVSLGMLYMPKYIILFHDEQVPRK 857
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
Qy 715 QPNVQFC-IVALVI-I-FCSTITLCLVFPVKLITLTNPDAATONRR 758
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
RESULT 11
ID R72095 standard; Protein: 481 AA.
AC R72095;
DT 26-SEP-1995 (first entry)
DE Human mglur7 clone cmr5.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KM signal transducer.
OS Homo sapiens.
PN MO9508627-A.
PD 30-MAR-1995.
PE 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016553.
PA (CIBA ) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetzner I;
PI WPI; 95-139596/18.
DR N-PSDB; Q89345.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PS Clads, which modulate signal transduction activity
PS Claim 8; Page 69-72; 110pp; English.
CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA
CC clones were isolated from cDNA libraries using a rat mglur4 probe.
CC Fetal brain partial cDNA clone cmr5, encoding the protein given in
CC R72095, was obtained. The missing 5' region of the clone was
CC generated by PCR from brain cDNA. Sequence comparison of fetal
CC brain and hippocampus clones indicated the existence of 2 subtypes
CC of hmglur7 (R72097-98).
SQ Sequence 481 AA;
```

```
Query Match 3.1%; Score 214; DB 1; Length 481;
Best Local Similarity 22.9%; Pred. No. 3.67e-06;
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;
```

```
Db 172 LAMGLII-ATTFVWATPIRYNDPIVKSAGRELSYVLAGIFLCY--ITF-L--MIA- 223
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 487 LTILGIMASAFLEFN-IKNRNOKLIKMSPPYNNLIIIGMLSYASIFLEGLDSFVS 545
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 224 KPDVAVSFRVFLGCMCSYVALLTKNRIYRIPEQGRKSTARLISPTQSQAITS 283
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 546 KTFETLCTVIRKWTWLTWGYTAFGAMFAKTWRHAIRKNVAK-K--KIIRDOKLVI 602
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 284 LISVQLGVEI-WFQVDPNIIID-YD-EKTKNPEQA-RGYLK-CDITDQI-ICSL-G 336
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 603 MLILDL-CILICWQAVDPLRRTYERYSMEPDPAGRDISIRPLEHCENHTMTWLG 661
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 337 YSILLV-TC-TVYAIKTRGVPEFTEANRPIGFTMTTCIVWLAFIPFEGTAQSAE 394
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 662 YKGLMLFCGFLAMETRNVSIPA-LNDSKYIGMSYVNGIMCIIIGAASFRTDQPN 720
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 395 IQTTLITISMLLSASVSLGMLYMPKYIILFHPELVNQKRKSE 438
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 721 C-IVALVI-I-FCSTITLCLVFPVKLITLTNPDAATONRRQF 761
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
RESULT 12
ID R72093 standard; Protein: 867 AA.
AC R72093;
DT 26-SEP-1995 (first entry)
DE Human mglur7 clone cmr2.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KM signal transducer.
OS Homo sapiens.
PN MO9508627-A.
PD 30-MAR-1995.
PE 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016553.
PA (CIBA ) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetzner I;
```

CC glutamatergic ligands. Its amino acid sequence was determined from
CC cDNA clones (see also T38322) obt'd. from a human retinal cDNA library.
CC A splice variant has an alternative N-terminal sequence (see also
CC W01100). Recombinant receptors, practically free of contamination
CC by other receptors, can be produced in host cells. The receptors,
CC and cells expressing them, are used in drug screening to identify
CC cpds. that modulate mGluR6.
SQ Sequence 877 AA;

Query Match 3.3%; Score 225; DB 1; Length 877;
Best Local Similarity 21.5%; Pred. No. 5,82e-07;
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

Db 592 LAVGIATTTVAATVVRNNDPIVRSAGRELSVLLTGIFLYA-I-TF-L--WVAP 645
Y 487 LTIIGIMASAFLEFNKKNOKLIKSSPYNNLLIIGMLSYASIFLFGDGSFVSK 546
Db 646 G-AVCAARLEFLGGLTISYSLTKNTIYIFEQGKRSVTPPPFISQVITFSL 704
Y 547 TFEFLCTVRWILTVGTTAFGAMFAKFWVHAIFKNVK--MKKK-IIRDOKLVIYVGM 603
Db 705 TSIQVGMIMLGAARPHSVYID-YE-EQRTVDEPA-RGYLK-CDMSDSL-IGCL-GY- 757
Y 604 LLLDCLICWQAVDPURRTVERYSMEPPDAGDISIRPLEHCENTHMTWIGIYAYK 663
Db 758 SLLMWTC-TVYAKRGVPEFNEAKPIGFMTTCIIMLAFVPIFGTAQSAEKMYI 816
Y 664 GLMLFGCFIAMETRVNSIP-ALNDSKIYGMYSYNGVICIIGAAVSFLTRQPNVQFC- 721
Db 817 TTTITVMSLSASVSLGMLYMPKVTYIIFHPEDNVOKRR 855
Y 722 IVALVI-I-FCSTITLCLVFPKLTILRTPNDAQNRR 758

RESULT 8
ID W49928 standard; Protein; 908 AA.
AC W49928;
DT 09-JUN-1998 (first entry)
DE Human metabotropic glutamate receptor (mGluR).
KW Metabotropic glutamate receptor; mGluR; screening; stroke; epilepsy;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
OS Homo sapiens.
PN W09748724-R2.
PD 24-DEC-1997.
PE 20-FEB-1997; U09025.
PR 21-FEB-1994; US-604298.
PA (NPSF-) NPS PHARM INC.
PI Fuller FH, Hammett LG, Simin RT, Stormann TW.
DR WPI: 98-063076/06.
N-PSDB: V17116.
PT Novel human metabotropic glutamate receptor - for screening
PT compounds useful for treating e.g. stroke, epilepsy or diseases such
PT as Alzheimer's, Parkinson's or Huntington's diseases
PS Claim 7; Fig 1; 98pp; English.
CC This is a novel human metabotropic glutamate receptor (mGluR). A
CC purified or isolated nucleic acid of at least 15 nucleotides in length
CC encoding at least 6 contiguous amino acids of the unique portion of this
CC mGluR can be used to generate transgenic mammals by insertion of the
CC nucleic acid into the mammalian genome. The mGluR can be used to screen
CC for compounds which modulate its activity, especially in the
CC physiological functions of convulsions, neuroprotection, neuronal death
CC and development, central control of cardiac activity, waking, control of
CC movement and control of vestibulo-ocular reflex. Such compounds can be used
CC to treat glutamate excitotoxicity, global and focal ischemic and
CC haemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced
CC nerve damage, epilepsy or neurodegenerative diseases such as Alzheimer's,
CC Parkinson's or Huntington's diseases.
SQ Sequence 908 AA;

Query Match 3.3%; Score 231; DB 1; Length 908;
Best Local Similarity 21.9%; Pred. No. 2.12e-07;
Matches 62; Conservative 97; Mismatches 100; Indels 24; Gaps 21;

Db 590 VALIGII-ATTEVIVTVVRNNDPIVRSAGRELSVLLTGIFLCYSITFLM-I-AA--PD 644
Y 487 LTIIGIMASAFLEFN-IKNNOKLIKSSPYNNLLIIGMLSYASIFLFGDGSFVSE 545
Db 645 -TI--ICSFRRVFLGGLGCSYAAALTKNTIYIFEQGKRSVTPAPFISPASQVITFS 701
Y 546 KTFEFLCTVRWILTVGTTAFGAMFAKFWVHAIFKNVK-K--KIRDOKLVIYVGM 602
Db 702 LISVOLLGVEYFVDDPHIID-YG-EQRTVDEPA-RGYLK-CDISDSL-IGSL-GY 755
Y 603 MLLDCLICWQAVDPURRTVERYSMEPPDAGDISIRPLEHCENTHMTWIGIYAY 662
Db 756 SLLMW-TC-TVYAKRGVPEFNEAKPIGFMTTCIIMLAFVPIFGTAQSAEKMYI 813
Y 663 KGLMLFGCFIAMETRVNSIP-ALNDSKIYGMYSYNGVICIIGAAVSFLTRQPNVQFC 721
Db 814 OTTITVMSLSASVSLGMLYMPKVTYIIFHPEDNVOKRRSF 856
Y 722 IVALVI-I-FCSTITLCLVFPKLTILRTPNDAQNRRFOF 761

RESULT 9
ID R82658 standard; protein; 912 AA.
AC R82658;
DT 20-DEC-1995 (first entry)
DE Human mGluR4.
KW Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;
KW Alzheimer disease; detection; diagnosis; therapy.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT domain
FT /label= TMD-I
FT /note= "transmembrane domain I"
FT 625..645
FT /label= TMD-II
FT /note= "transmembrane domain II"
FT 657..675
FT /label= TMD-III
FT /note= "transmembrane domain III"
FT 699..720
FT /label= TMD-IV
FT /note= "transmembrane domain IV"
FT 751..771
FT /label= TMD-V
FT /note= "transmembrane domain V"
FT 786..807
FT /label= TMD-VI
FT /note= "transmembrane domain VI"
FT 823..847
FT /label= TMD-VII
FT /note= "transmembrane domain VII"
PN W09522609-A2.
PD 24-AUG-1995.
PE 21-FEB-1995; G00356.
PR 21-FEB-1994; GB-003285.
PR 01-AUG-1994; GB-015532.
PA (WEIL) WEILCOHE FOUND LTD.
PI Makoff AJ.
DR WPI: 95-302715/39.
N-PSDB: T03888.
PT New isolated human metabotropic glutamate receptors - used for
PT detection, diagnosis and therapy of diseases associated with the
PT receptors, eg. stroke, epilepsy and Alzheimer's disease.
PS Claim 2; Page 40-43; 55pp; English.
CC mRNA from the human cerebellum was used to construct a cDNA
CC library. cDNA was amplified by PCR primers (T03896-97) based on rat
CC mGluR4 sequences and with the primers given in T03898-99 to obtain
CC cDNA encoding human mGluR4.
SQ Sequence 912 AA;

Query Match 3.3%; Score 228; DB 1; Length 912;
Best Local Similarity 21.6%; Pred. No. 3.51e-07;
Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

Query Match	24.3%;	Score 1680;	DB 1;	Length 844;
Best Local Similarity	35.1%;	Pred. No. 4.32e-126;		
Matches	262;	Conservative 192;	Mismatches 269;	Indels 23;
			Gaps	21

RESULT	4
ID	W40116 standard; Protein; 960 AA.
AC	W40116;
DT	03-JUN-1998 (first entry)

Query Match 24.2%; Score 1672; DB 1; Length 960;
Best Local Similarity 36.0%; Pred. No. 2.04e-125;
Matches 248; Conservative 177; Mismatches 247; Indels 16; Gaps 14.

Dd	184	GOACOPPEVALEADVRSRDILPDVELLHNSKCPGATVYELLYNDPIKILMP	24
Qy	73	GRVLPAVELATIQIRNE-SILRPYFLIDRLYDECDMAKGLKAFDAIKYGNHIAWFG	133
Dd	244	G-CGSYSTVLAEAARKMNLYLVSSSSPALSNQRPTFRHRBSATILHNTRYKLEK	30
Qy	132	GVCSYSTVLAESLOGMNLYLVSSFPATTPVADKKIPEYFRVPSDANVANPAILLK	191
Dd	303	MGWKIATIQTEVFTSTDLDEREVAEAIETFPQSFSDPAPVANKLRQDARIIV	362
Qy	192	FRMRVFTLRQDQRESRBNLDVGLXGEDIEJSDTESNDPCTSVYKILKGNVRIIL	25
Dd	363	GLEFENARVCEPYKKELEPEKKYVWFLJGMYADNMF-KTY-DP-SINCYKEMTEAVE	411
Qy	252	GQPDNMAKAVFCQAEBSMEFSKOWITIPWIEPAMWEOVHEANSSCLRRSLAAME	311
Dd	420	GHTTEIYMLNPANTRSISNMTSOEFYEKILKRLRHRETEGFOEAPILADYALWALA	473
Qy	312	GYIVDEEPLSKOLKTINGKTPQOY-EREYNS-KRSGVPSKFH-G-YAYGIVWIAKT	367
Dd	480	LNRKSSG--GGRSGVLEFENYNNNTINDOYRAMNSSFEGYSGHYVADSGSAMTL	533
Qy	368	LQRMETLHANSRHOIRQDENTHTDKILLANMANNTNFGYGGVAV-RNGEMGIK	422
Dd	538	IEOLGGSYKRIIGYDSTKDLISW-SKTDWKIGSGPADDTLYIKITFRLSQKLEISV	599
Qy	427	ETFOQDREKYGVEYAAVADTLEIINDIPROGSEPRDKTILLEDLRKISPLYSILSA	486
Dd	597	LSSIGIYLAVCCSPENYVSHRYVONSOPRLNLTAVGCSLAAVPLRGLGDGHISRS	656
Qy	487	LTLIGMASAFLEFIKRNKROKLIKMSPPMNNLLILGMSLYASILEFLYDGSFVSEK	544
Dd	657	QEPFVCOARLWELGJFSLGYSMFKIMWVHTFKREKKEKWRKTEPMRLVATGLL	716
Qy	547	TFEFLICVTRWILTYGTTAFGAMAKRWYHAIF--KNYKMK-KKIIIDOKLIVYGM	603
Dd	717	VGMQVYLAITWOVPLHNTIKTEKKEPRKDDIVYLPDEHSSCKKNWMLGYFYUK	779
Qy	604	LINDCLITGMQAVDPIKRTYVRSKSMEDPAGRGRISTRPILLECENHTHTWGLGIVAYK	666

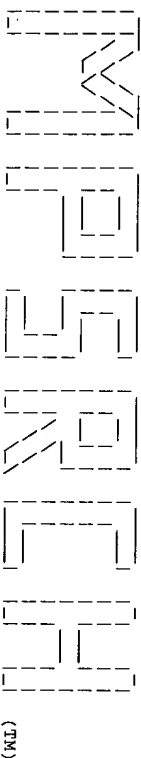
QY 161 VLADKKYFFFTVSDNANVPAIIKLKHFWRNRVGLTIDVQRFSEVRNDLIGVLYG 220
DB 216 AGIEITFRQSFSDPAVPVKNLKRQDARIIVGLFEYFEARKYCEYKRELGKKYVPEL 275
QY 221 EDIEISTEFSFSDPCSVYKLLKGNVRIITLGGFDONMAKAVCAFEISMESGSKWMI 280
DB 276 IGVYADNMF-KIY-DP-SINCIYDEMTAEVGHITTEIYMLNPANTRSISNMTSQEVEK 332
QY 281 PGWTEPAMWQVHVEANSRCLRRSLAAAMEGYIGVDFEPLSSKQIKTISGKTPQOY-ER 339
DB 333 LTRLRKHPEETGGFOAPALAYDAIMALALAKTSSG--GGRSGVRLEDENNNTIJD 390
QY 340 EYNS-KRSGVGSPKFEH-G-YAYDGIWIAKTLQRAEETHLHASSRHORIODENTDHTLCK 396
DB 391 QIYRAMSSSEFGVSGHVFEDASGRMAWTLIEOLGGSYKKIGYDSTKDLGSM--SKTD 449
QY 397 IILNANETNEFGVYGQVVF-RNGERMGTIKFTQFODSREVKKGEYNAVADLEIINDTI 455
DB 450 KWIIGSPADQTLVYKTFEFLSOKLFISVSLGIVLAVCLSFNINSHVRIYQNSQ 509
QY 456 RFQSGSEPKDKTIIIEQLRKISLPLYSILSALTILGIMASAFLEFNKRNOKLIKMS 515
DB 510 PNLNLTAVGCSLALAVPFLGDIYHIGNOPFVGOARLWMLLGESLGYGSMFTKIM 569
QY 516 PYMNNLTILGKMSYASIFLGLDGSFVSEKTEETCTVTFWTLVGYTAFGAMFAKIM 575
DB 570 WHTVETFKKEKKEMRKLTLEPKLYATVGLVGMVLTLLAIWQIVDPILHRTIETFAKEEP 629
QY 576 RVHAIIF--KNVKKM-KKIINDQKLLVIGGMLLIDLCILCQWAVDPLRRTVRYSMEDP 632
DB 630 KEDIVSILPOLHEGSSRRKMTWLIGIFYGKLLILGIFLAVETYSVSTEKINDHRANG 689
QY 633 PAGRDISIRPLEHCENTHMTIWLGIYVAYKGLMLFGCLAMEIRNVASIPALINDSKYIG 692
DB 690 MAIYNVAVLCITPYMMLISSQODAAFAFASALIAVSSYITLVLFVPMRRLIRGE 748
QY 693 MSYVNGIMCTIGAASVFLTRDPNVQFCIVALIIFCSITTLCLVFPKLTITLRTPD 751

RESULT 2
ID W40117 standard; Protein: 793 AA.
AC W40117;
DE Human GABA-BR1a/D receptor protein.
KW GABA-aminobutyric acid; GABA-BR1a/D receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
OS Homo sapiens.
PN MO9746675-A1.
PD 11-DEC-1997.
PE 19-MAR-1997: E01370.
PR 22-NOV-1996: US-756091.
PR 30-MAY-1996: US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR N-PSDB: V10265.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 4: Page 62-67; 108pp; English.
CC This sequence represents a novel human GABA-B receptor protein,
CC GABA-BR1a/D. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
DR N-PSDB: V10265.
Sequence 793 AA;

Query Match 24.3%; Score 1676; DB 1; Length 793;

Best Local Similarity 36.0%; Pred. No. 9.38e-126;
Matches 248; Conservative 179; Mismatches 245; Indels 16; Gaps 14;
DB 17 GOACPAVEMLEEVNSRDILIPYELKLIIHDSKCDPGQATYLYELLYNDPIKILMP 76
QY 73 GRGVLPANELAIEQIRNE-SILRREYFLDLRLYDECNAGLAFYALIKYGNHLMVFG 131
DB 77 G-CSSVSTLVAEARMMNLIVLSYSSSPALSNRQRPETFEFRHPHSATLHPRVKLEEK 135
QY 132 GVCPSVTIIESLOGWMLVOLSFPAATPVLADEKKKPYFEFRVPSDNANVPAIIKLK 191
DB 136 MGWKIATIQOTTEVFTSLDDEERKREAGIETTFQSFSDPAVPVKNLKRQDARIIV 195
QY 192 FRWRVGTITDVOFRFSVRNDLIGVLDGEDIETSDTESNDCTISYKLLKGNVRIIL 251
DB 196 GLFEYFEARKYCEYKRELGKKYVPELIGVYADNMF-KIY-DP-SINCIYDEMTAEV 252
QY 252 GQFQONMAAKYFCCAFESMGSCKYQWIIIPWYEPAMWQVHVEANSRCLRRSLAAAME 311
DB 253 GHITTEIYMLNPANTRSISNMTSQEVEKTLRLKRHPETGGFOAPALAYDAIMALALA 312
QY 312 GYIGVDFEPLSSKQIKTISGKTPQOY-EREYNS-KRSGVGSPKFEH-G-YAYDGIWIAK 367
DB 313 LNKTSIG--GGRSGVRLEDENNNTIJDQIYRAMSSSEFGVSGHVFEDASGRMAWTL 370
QY 368 LQRAEETHLHASSRHORIODENTDHTLCKIILNANETNEFGVYGQVVF-RNGERMGTIK 426
DB 371 IEOLGGSYKKIGYDSTKDLGSM--SKTDKWIIGSPADQTLVYKTFEFLSOKLFISV 429
QY 427 FTQFODSREVKKGEYNAVADLEIINDTIRFQSGSEPKDKTIIIEQLRKISLPLYSILSA 466
DB 430 ISSIGIVLAVCLSFNINSHVRIYQNSQPNLNLAVGCSLALAAVPLGDIYHIGN 489
QY 487 LITLGMASAFLEFNINRNOKLIKMSPPYNNLIIIGMLYASIFLGLDGSFVSEK 546
DB 490 QFFPYQCARMLNLGSGFSLGYSMTKIMWHTVETFKKEKKEMRKLTLEPKLYATVGL 549
QY 547 TFEETCTVTFWTLVGYTAFGAMFAKIMRVHAIIF--KNVKKM-KKIINDQKLLVIGGM 603
DB 550 VGMVLTLLAIWQIVDPILHRTIETFAKEEPKEDIVSILPOLHEGSSRRKMTWLIGIFYGK 609
QY 604 LIIDLCILCQWAVDPLRRTVRYSMEDPAGRDISIRPLEHCENTHMTIWLGIYVAYK 663
DB 610 GLLILGIFLAVETYSVSTEKINDHRANGMAIYNVAVLCITAPYTMILSSQODAAFAFA 669
QY 664 GLIMFGCEFLAMEIRNVASIPALINDSKYIGMVICIGAASVFLTRDPNVQFCIV 723
DB 670 SLATYFSSYITLVLFVPMRRLIRGE 697
QY 724 ALVLIIFCSITTLCLVFPKLTITLRTPD 751

RESULT 3
ID W40118 standard; Protein: 844 AA.
AC W40118;
DE 03-JUN-1998 (first entry)
DE Rat GABA-BR1b receptor protein.
KW GABA-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
OS Rattus norvegicus.
PN MO9746675-A1.
PD 11-DEC-1997.
PE 19-MAR-1997: E01370.
PR 22-NOV-1996: US-756091.
PR 30-MAY-1996: US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR N-PSDB: V10265.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders



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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Mar 15 21:49:17 2000; Maspar time 32.56 Seconds
Tabular output not generated. 683.720 Million cell updates/sec

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Perfect Score: 6906
Sequence: 1 NASPPSSGQPRPPPPPPPPA.....TASPRHRHVPSPFRVMSGL 940

Scoring table:
PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 39.909; Variance 201.597; scale 0.198

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1684	24.4	844	1 W40119	Human GABA-BR1b recept	1.99e-126
2	1676	24.3	793	1 W40117	Human GABA-BR1a/b rece	9.38e-126
3	1680	24.3	844	1 W40118	Rat GABA-BR1b receptor	4.32e-126
4	1672	24.2	960	1 W40116	Rat GABA-BR1a receptor	2.04e-125
5	267	3.9	38	1 Y13091	Human secreted protein	4.52e-10
6	232	3.4	908	1 W41368	Human metabotropic glu	1.79e-07
7	225	3.3	877	1 W01099	Metabotropic glutamate	5.82e-07
8	231	3.3	908	1 W49928	Human metabotropic glu	2.12e-07
9	228	3.3	912	1 R82658	Human mglur4.	3.51e-07
10	228	3.3	912	1 R72092	Human mglur7 clone cmr	3.67e-06
11	214	3.1	867	1 R72093	Human mglur7 clone cmr	3.67e-06
12	214	3.1	867	1 R72093	Human mglur7a.	2.22e-06
13	217	3.1	915	1 R72097	Human mglur7a.	2.22e-06
14	214	3.1	915	1 R80479	Rat metabotropic gluta	3.67e-06
15	214	3.1	922	1 R72098	Human mglur7b.	3.67e-06
16	204	3.0	1026	1 W38259	Dogfish shark kidney c	1.92e-05
17	199	2.9	1079	1 W94928	Rat kidney cell calculi	4.39e-05
18	199	2.9	1079	1 W94928	Rat kidney extracellular	4.39e-05
19	199	2.9	1079	1 W54847	Rat kidney calcium rec	4.39e-05
20	199	2.9	1079	1 W89566	Rat parathyroid calculi	1.17e-04
21	193	2.8	872	1 R89580	Metabotropic glutamate	9.95e-05
22	194	2.8	1078	1 W89565	Human parathyroid calc	9.95e-05
23	194	2.8	1078	1 W11869	Parathyroid calcium re	9.95e-05

24	194	2.8	1078	1 W54846	Human parathyroid calc	9.95e-05
25	194	2.8	1078	1 W38274	Human parathyroid cell	9.95e-05
26	192	2.8	1085	1 W38272	Bovine parathyroid cell	1.38e-04
27	192	2.8	1085	1 W54844	Bovine parathyroid cal	1.38e-04
28	192	2.8	1085	1 W89563	Bovine parathyroid cal	1.38e-04
29	194	2.8	1088	1 W89564	Human parathyroid calc	9.95e-05
30	194	2.8	1088	1 W11888	Parathyroid calcium re	9.95e-05
31	194	2.8	1088	1 W38273	Human parathyroid cell	9.95e-05
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33	194	2.8	1219	1 W25763	Amino acid sequence of	1.33e-03
34	184	2.7	872	1 R95052	Human metabotropic glu	5.06e-04
35	188	2.7	877	1 R82657	Human mglur3.	2.65e-04
36	188	2.7	879	1 R64252	Human mglur3.	2.65e-04
37	184	2.7	1180	1 R64253	Human mglur5a.	5.06e-04
38	184	2.7	1180	1 R64254	Human mglur5b.	5.06e-04
39	181	2.6	779	1 W94921	Rat pheromone receptor	8.21e-04
40	178	2.6	906	1 R64250	Human mglur1b.	1.33e-03
41	178	2.6	906	1 R25081	GLU-G-R subtype 1b.	1.33e-03
42	178	2.6	1056	1 W25765	Amino acid sequence of	1.33e-03
43	178	2.6	1056	1 W25764	Amino acid sequence of	1.33e-03
44	178	2.6	1058	1 W25762	Amino acid sequence of	1.33e-03
45	178	2.6	1199	1 R25080	GLU-G-R subtype 1a.	1.33e-03

ALIGNMENTS

RESULT 1	ID	W40119	standard; protein; 844 AA.
AC	W40119	03-UN-1998	(first entry)
DT	03-UN-1998	Human GABA-BR1b receptor protein.	
DE	Human GABA-BR1b receptor protein.	Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;	
KW	inhibitory neurotransmitter; peripheral nervous system; antagonist;		
KW	treatment; dementia; depression; anxiety; bronchial inflammation; asthma;		
KW	epilepsy; cognitive function.		
OS	Homo sapiens.		
PN	W09746675-A1.		
PD	11-DEC-1997.		
PF	19-MAR-1997; E01370.		
PR	22-NOV-1996; US-756091.		
PR	30-MAY-1996; US-655716.		
PA	(NOVS) NOVARTIS AG.		
PI	Bettler B, Bitliger H, Froestl W, Kaupmann K, Mickel SJ.		
DR	WPI; 98-042183/04.		
DR	N-PSDB; V10267.		
PT	Purified GABA-B receptor or receptor protein - and antagonists of		
PT	these which may be useful in treating nervous system disorders		
PS	Claim 4; Page 86-90; 108pp; English.		
CC	This sequence represents a novel human GABA-B receptor protein,		
CC	GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory		
CC	neurotransmitter found in the brain and peripheral nervous system		
CC	and this receptor may be used for the identification of GABA-B		
CC	receptor agonists and antagonists. Such proteins may be used in		
CC	treatment of dementia, depression, anxiety, epilepsy, spasticity,		
CC	bronchial inflammation or asthma or to improve cognitive function.		
CC	GABA-B receptor ligands and probes derived from this sequence can be		
CC	used to assay for GABA-B receptors or DNA encoding them.		
CC	Sequence 844 AA;		

Query Match 24.4%; Score 1684; DB 1; Length 844;
Best Local Similarity 35.3%; Pred. No. 1.99e-126;
Matches 254; Conservative 191; Mismatches 255; Indels 19; Gaps 17;

Db	40	SRVPPSSERRRAYIGALFPMG-G-GMPG-GQACQAVEMALEDVNSRDIDPDIYKLK 96
Oy	42	TRGAPRPSSPPUSLWMLPLTREVAKSGISGRVLAVALAEIIOINNE-SLRPPFIDL 100
Db	97	IHDSCDPCGQATKYLIELYNDPIKIIIMP-G-SSYSTVAEARWMTIVSYGSSP 155
Oy	101	RLYTECDNAGKLAFAFDALIKYGNHLMVGGVCPSTSTIAESLQWNIWQSFATTP 160
Db	156	ALSNRQRPFFRFPATLHNPTRVLFERWKKIATIQQTTEVTSTLDDLEERVKE 215

Tue Mar 21 10:26:14 2000

US-09-211-755-4.rai

Page 10

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CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1085 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1085 AA; 121170 MW; 6189757 CN

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Query Match	2.8%	Score 192	DB 1	Length 1085
Best Local Similarity	27.5%	Pred. NO.	9.18E-05	
Matches	25	Conservative	32	Mismatches 34; Indels 0; Gaps 0;
Db	126	LD6CNCSEHISTAVYANGSGISTAVNALLGFIPIYQVASSSRLLSKNKNFSEL	185	
Qy	113	LKAFYDPIKRGPHMLVGGVCPSTVSLAESLOGNMUVDLSFAATTPLAAKKRPIFF	172	
Db	186	RTIPNDEHQATMADIIIEFFRNMYGTIAAD	216	
Qy	173	RTVPDSNAVNPALKLKLKHEFRKRRVGLTQD	203	

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Job time : 36 secs.

Search completed: Wed Mar 15 22:32:13 2000
Job time : 36 secs.

OY 173 RTVPSDNAVNPALIKLKHFRRRVGTITOD 203

RESULT 14 STANDARD: PRT: 1085 AA.

ID US-08-480-751-5

Sequence 5, Application US/08480751

Patent No. 5858684

GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth

APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert

APPLICANT: Forrest H. Fuller

APPLICANT: James E. Garrett, Jr.

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,751

FILING DATE: 7 June, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/834,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 213/004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1085 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SO SEQUENCE 1085 AA; 121170 MW; 6189757 CN;

Query Match

Best Local Similarity 27.5%; Score 192; DB 2; Length 1085;

Matches 25; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

Db

126 LDEFNCSEHPISTIVAVGATGSGISTAVANLIGFYIPQVSYASSRLSNKPKSF 185

OY 113 LKAFYDAIKYCPNHLNMFEGVCPSVTSIIASLGQWNLVQSFATPTVADKKKPYPF 172

Db

186 RTVPSDNAVNPALIKLKHFRRRVGTITAD 216

OY 173 RTVPSDNAVNPALIKLKHFRRRVGTITOD 203

RESULT 15

ID US-08-484-565-5 STANDARD: PRT: 1085 AA.

XX US-08-484-565-5

AC xxxxxx

DT

DE

XX

Sequence 5, Application US/08484565

Patent No. 5763569

GENERAL INFORMATION:

APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert

APPLICANT: James E. Garrett, Jr.

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,565

FILING DATE: 7 June, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/834,044

FILING DATE: 11 February, 1992

CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1078 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
Query Match 2.8%; Score 194; DB 1; Length 1078;
Best Local Similarity 28.6%; Pred. No. 6.67e-05;
Matches 26; Conservative 31; Mismatches 34; Indels 0; Gaps 0;
Db 125 LDEFCNCSEHIPSTIAVVGATGSGVSTAVANLGLFYIPQVSYASSSRLLSNKNQKFSFL 184
QY 113 LKAFYDAIKYGNHLMVFGVCPSTVSTIAESLQGMNLVLSFAATPVADKKRKYFF 172
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QY 173 RTVPSDNAVNPAILKLKLFRRMRVGTITQD 203
XX
DT
XX
AC xxxxxx
ID US-08-485-588-7 STANDARD; PRT; 1078 AA.
XX
XX
Sequence 7, Application US/08485588
CC Patent No. 5688938
CC GENERAL INFORMATION:
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: Forrest H. Fuller
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCITUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/485,588
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application

CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/005
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1078 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
Query Match 2.8%; Score 194; DB 1; Length 1078;
Best Local Similarity 28.6%; Pred. No. 6.67e-05;
Matches 26; Conservative 31; Mismatches 34; Indels 0; Gaps 0;
Db 125 LDEFCNCSEHIPSTIAVVGATGSGVSTAVANLGLFYIPQVSYASSSRLLSNKNQKFSFL 184
QY 113 LKAFYDAIKYGNHLMVFGVCPSTVSTIAESLQGMNLVLSFAATPVADKKRKYFF 172
Db 185 RTIPNDEHQATAMADIEYFRMNVGTIAAD 215
QY 173 RTVPSDNAVNPAILKLKLFRRMRVGTITQD 203
XX
DT
XX
AC xxxxxx
ID US-08-480-751-7 STANDARD; PRT; 1078 AA.
XX
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Sequence 7, Application US/08480751
CC Patent No. 5838684
CC GENERAL INFORMATION:
CC APPLICANT: Edward F. Nemeth
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: Forrest H. Fuller
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCITUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street

CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,565
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;
SQ
Query Match 2.9%; Score 199; DB 1; Length 1079;
Best Local Similarity 29.7%; Pred. No. 3.01e-05;
Matches 27; Conservative 30; Mismatches 34; Indels 0; Gaps 0;
Db 125 LDFCNCSEHPSITAVGATGSGVSTAVANLGLFIPIQVSYASSSRLLSNKNQYKSF 184
QY 113 LKAFYDAIKYGNHLMVFGVCPSTVSIIESLOGWNLVQLSFATTPVLADKKKYYFF 172
Db 185 RTIPNDEQATAMADIIIEYFRWNVGTIAD 215
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XX
AC xxxxxx
XX
DT
XX
DE Sequence 8, Application US/08485588

XX
CC Sequence 8, Application US/08485588
CC Patent No. 5688938
CC GENERAL INFORMATION:
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: Forrest H. Fuller
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/485,588
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/005
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;
SQ
Query Match 2.9%; Score 199; DB 1; Length 1079;
Best Local Similarity 29.7%; Pred. No. 3.01e-05;
Matches 27; Conservative 30; Mismatches 34; Indels 0; Gaps 0;
Db 125 LDFCNCSEHPSITAVGATGSGVSTAVANLGLFIPIQVSYASSSRLLSNKNQYKSF 184
QY 113 LKAFYDAIKYGNHLMVFGVCPSTVSIIESLOGWNLVQLSFATTPVLADKKKYYFF 172

CC FILING DATE: 30-DEC-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Parmelee, Steven W.
 CC REGISTRATION NUMBER: 31,990
 CC REFERENCE/DOCKET NUMBER: 13952-18-2
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 206-467-9600
 CC TELEFAX: 415-576-0300
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 915 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;
 SQ
 Query Match 3.1%; Score 214; DB 1; Length 915;
 Best Local Similarity 22.9%; Pred. No. 2.72e-06;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;
 Db 597 LAMGII-ATIFVATFIRYNDTPIVRASGRELSVLTGIFLCY--ITF-L---MIA- 648
 Qy 487 LTIIGMNASAFLEFN-IKRNOKLIKSSPYNNLLIIGMLSYASIFLFGDGSFVSE 545
 Db 649 KPDVAVCSFRFVTLGLMCISYALLTKTNRIYRIFEOGKSVTAPRLISPTSQLAITSS 708
 Qy 546 KTFETLCTVFTWLTGTYTAFGAMFAKTWRVHAIFNNVKK-K-KIIDOKLTVYVG 602
 Db 709 LISVOLGVEL-WGVDPNPIIID-YD-EHKYNNPEQA-RGVLK-CDITDLOI-ICSL-G 761
 Qy 603 MLTIDL-CILICQWADVPLRRTVERYSMEPDPAGRDISIRPLEHCENHTMTWLCIYVA 661
 Db 762 YSILIMV-TC-TYVAIKTRGVENENAKPIGFTMTYTCIWMLAIFPIFGTAQSAEKLY 819
 Qy 662 YKGLIMFGCFLAWEIRNVSIPA-LNDSKITGMSVYVWGIMCIIGAASVLTROQNVQF 720
 Db 820 IQTTLTISNLSASVALGMLYMPKYYIIIFHPELVNOKRRSF 863
 Qy 721 C-IYALVI-I-FCSITILCLVFEVFKLITLRTNPDATQNRRFQF 761
 RESULT 4
 ID US-08-452-734A-2 STANDARD; PRT; 915 AA.
 AC xxxxxx
 DE Sequence 2, Application US/08452734A
 XX Patent No. 5831047
 CC GENERAL INFORMATION:
 CC APPLICANT: Segerson, Thomas P.
 CC APPLICANT: Kinzie, J. Mark
 CC APPLICANT: Mulvihill, Eileen R.
 CC APPLICANT: Saugstad, Julie A.
 CC APPLICANT: Westbrook, Gary L.
 CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
 CC NUMBER OF SEQUENCES: 5
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, 8th floor
 CC City: San Francisco
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94111-3834
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/452,734A
 CC FILING DATE: 30-MAY-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/176,401
 CC FILING DATE: 30-DEC-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Parmelee, Steven W.
 CC REGISTRATION NUMBER: 31,990
 CC REFERENCE/DOCKET NUMBER: 13952-18-1
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 206-467-9600
 CC TELEFAX: 415-576-0300
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 915 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;
 SQ
 Query Match 3.1%; Score 214; DB 2; Length 915;
 Best Local Similarity 22.9%; Pred. No. 2.72e-06;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;
 Db 597 LAMGII-ATIFVATFIRYNDTPIVRASGRELSVLTGIFLCY--ITF-L---MIA- 648
 Qy 487 LTIIGMNASAFLEFN-IKRNOKLIKSSPYNNLLIIGMLSYASIFLFGDGSFVSE 545
 Db 649 KPDVAVCSFRFVTLGLMCISYALLTKTNRIYRIFEOGKSVTAPRLISPTSQLAITSS 708
 Qy 546 KTFETLCTVFTWLTGTYTAFGAMFAKTWRVHAIFNNVKK-K-KIIDOKLTVYVG 602
 Db 709 LISVOLGVEL-WGVDPNPIIID-YD-EHKYNNPEQA-RGVLK-CDITDLOI-ICSL-G 761
 Qy 603 MLTIDL-CILICQWADVPLRRTVERYSMEPDPAGRDISIRPLEHCENHTMTWLCIYVA 661
 Db 762 YSILIMV-TC-TYVAIKTRGVENENAKPIGFTMTYTCIWMLAIFPIFGTAQSAEKLY 819
 Qy 662 YKGLIMFGCFLAWEIRNVSIPA-LNDSKITGMSVYVWGIMCIIGAASVLTROQNVQF 720
 Db 820 IQTTLTISNLSASVALGMLYMPKYYIIIFHPELVNOKRRSF 863
 Qy 721 C-IYALVI-I-FCSITILCLVFEVFKLITLRTNPDATQNRRFQF 761
 RESULT 5
 ID PCT-US94-14989-2 STANDARD; PRT; 915 AA.
 AC xxxxxx
 DE Sequence 2, Application PC/TUS9414989
 XX Patent No. 5831047
 CC GENERAL INFORMATION:
 CC APPLICANT: Segerson, Thomas P.
 CC APPLICANT: Kinzie, J. Mark
 CC APPLICANT: Mulvihill, Eileen R.
 CC APPLICANT: Saugstad, Julie A.
 CC APPLICANT: Westbrook, Gary L.
 CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
 CC NUMBER OF SEQUENCES: 3
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/14989
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/176,401
 CC FILING DATE: 30-DEC-1993
 CC ATTORNEY/AGENT INFORMATION:

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MSEARCH protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Mar 15 22:31:37 2000; MasPar time 14.90 Seconds
Tabular output not generated. 817.556 Million cell updates/sec

(TM)

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Perfect Score: 6906
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Scoring table: PAM 150
Gap 11
Searched: 131253 seqs, 12956647 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-issued
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Statistics:

Mean 37.135; Variance 196.828; scale 0.189

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	199	2.9	1079	1	US-08-480-	Sequence 8, Applicatio	3.01e-05
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ALIGNMENTS

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Sequence 2, Application US/08407875
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CC Sequence 2, Application US/08407875
CC Patent No. 5912122
CC GENERAL INFORMATION:
CC APPLICANT: Daggett, Lorrie
CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
CC TITLE OF INVENTION: SUBTYPE mGLUR6, NUCLEIC ACIDS ENCODING SAME AND USES
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Pretty, Schroeder, Brueggemann & Clark
CC STREET: 444 South Flower Street, Suite 2000
CC CITY: Los Angeles
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/407,875
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: P41 9921
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-546-4737
CC TELEFAX: 619-546-9392
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 877 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein

Db	125	LDFEFCNCSEHIPSTIAVVGATGCGSVTAANILGLFIYPQVYASSSRLSNKNQYSFL	184
Qy	113	LKAFYDAIKRGPNHLMVFGVCSVSIINAESLQGNLVLSPFAATTPVLADKKKYPFF	172
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DATE	02-Jul-1996	#sequence_revision 02-Jul-1996	#text_change
ACCESSIONS	01-May-1998		
REFERENCE	159362; A55594		
#authors	Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.		
#journal	Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165		
#title	Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals.		
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#authors	Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.		
#journal	Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135		
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#accession	A53594		
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683-700	#domain transmembrane	#status predicted	#label TM2\
725-744	#domain transmembrane	#status predicted	#label TM3\
770-790	#domain transmembrane	#status predicted	#label TM4\
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841-860	#domain transmembrane	#status predicted	#label TM6\
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Query Match	2.9%;	Score 199;	DB 2; Length 1079;
Best Local Similarity	29.7%;	Pred. No. 3,47e-11;	
Matches	27; Conservative	30; Mismatches 34;	Indels 0; Gaps 0;
Db	125	LDFEFCNCSEHIPSTIAVVGATGCGSVTAANILGLFIYPQVYASSSRLSNKNQYSFL	184
Qy	113	LKAFYDAIKRGPNHLMVFGVCSVSIINAESLQGNLVLSPFAATTPVLADKKKYPFF	172
Db	185	RTIPNDEHQATAMADIEYFRMNVGTIAD	215
Qy	173	RTVPSDNAVNPALIKLKHFRMRVRGITLTD	203

QY	173	RTVSDNAVNPALIKLHKFRMRVGTLLQD	203
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ORGANISM	#formal_name Arabidopsis thaliana	#common_name mouse-ear cress	
DATE	23-Apr-1999	#sequence_revision 23-Apr-1999	#text_change 11-Jun-1999
ACCESSIONS	T05099		
REFERENCE	215398		
#authors	Beyan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, C. M.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.		
#submission	Submitted to the protein sequence Database, November 1998		
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Db	191	VPVYEN-NAEGEGIMPULDTALQAINIRIYRVIVISPNATDDEISVDLTLMTKPTFRV	249
QY	198	GLTLDQGRFE-VRNLDLTGLVIGDEIDIS-DRE-S-FSNDPETSVK-KLGNDRVRIIL	251
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DATE	19-Oct-1995	#sequence_revision 19-Oct-1995	#text_change 17-Mar-1999
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REFERENCE	A56715		
#authors	Garrett, J.E.; Capuano, I.V.; Hammetland, L.G.; Hung, B.C.P.		
#journal	Brown, E.M.; Hebert, S.C.; Nemeeth, E.F.; Fuller, F.		
#title	J. Biol. Chem. (1995) 270:12919-12925		
#cross-references	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.		
#accession	MUID:95279439		
##status	preliminary		
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738-759 #domain transmembrane #status predicted #label TM5\
773-794 #domain transmembrane #status predicted #label TM6\
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QY 624 VERISMEDPPAGRDI-SIRPLEHCENTHMTIWGIYAYKGLIMLFGC-FLAMETRNVS 681
Db 766 -ANENKAYIAFTWYTCIIMLAFVPI-YFGSNKRIITMCF-S-VSL-SATVALGCM-FV 819
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DATE 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
ACCESSIONS
REFERENCE
#authors Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
#journal Biochem. Biophys. Res. Commun. (1994) 199:1136-1143
#title Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.
#cross-references M01D:94197696
#accession JC2131
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KEYWORDS glycoprotein; neurotransmitter; receptor; transmembrane protein
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617-637 #domain transmembrane #status predicted #label TM2\
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DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 03-Aug-1995
ACCESSIONS S49341; A49419; C49419
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#authors Pearce, S.H.S.; Thakker, R.V.
#submision submitted to the EMBL data library, August 1994
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#authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.
#journal Cell (1993) 75:1297-1303
#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism.
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OY      144 GCCGCCCGAGCAGCCCGCGCTCTCCATCATATGGCCCTCATATGCCGCTACACAAGAAGTGCGC 203
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: Patent No. 5766880
: GENERAL INFORMATION:
: APPLICANT: Cole, Susan P.C.
: APPLICANT: Deeley, Roger G.
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OY	204	CAAGGCGACGATCGGGCGGCGGTGCTCCCGCG	238		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 09:33:48 ; Search time 6661.37 Seconds

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Scoring table: IDENTITY_NUC

Searched: 4846779 seqs, 2239806763 residues

Database : Pending_Patents_NA.*

Word size : 0

Number of hits that pass the threshold : 9693548

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5	2650.4	93.9	2652	1	PCT-US98-22033-3	Sequence 3, Appl1
6	2650.4	93.9	2652	1	PCT-US98-22033A-3	Sequence 3, Appl1
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10	2346.6	83.1	2826	1	PCT-US99-19651-46	Sequence 46, Appl1
11	2346.6	83.1	2826	42	US-09-211-755-46	Sequence 46, Appl1
12	2346.6	83.1	2826	52	US-09-390-134-30	Sequence 30, Appl1
13	2329.4	82.5	5787	87	US-60-172-373-2106	Sequence 28, Ap
14	2311	81.9	3396	1	PCT-US99-11869-28	Sequence 27, Appl1
15	2239.6	79.3	3399	1	PCT-US98-22033-1	Sequence 1, Appl1
16	2218.2	78.6	3244	1	PCT-US98-22033A-1	Sequence 1, Appl1
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SUMMARIES

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Oy	2581	CCCCAGCTCTCAATGTGAAACAGACGACGACGACCTCAAGAACATGCAAGAGCCCATAGAGAC	2640
Db	2581	CCCCAGCTCTCAATGTGAAACAGACGACGACGACCTCAAGAACATGCAAGAGCCCATAGAGAC	2640
Oy	2641	ATGAACCTCCCGGAGACATATCAACGCGCGGTGTGCTTCACAGCTCCCAATCTTCACACAC	2700
Db	2641	ATGAACCTCCCGGAGACATATCAACGCGCGGTGTGCTTCACAGCTCCCAATCTTCACACAC	2700
Oy	2701	GCCTACTCCCATTCATCGATCGAGGCGGTGATGCCAGTSCGTACGCCCTGTGTACCCCT	2760
Db	2701	GCCTACTCCCATTCATCGATCGAGGCGGTGATGCCAGTSCGTACGCCCTGTGTACCCCT	2760
Oy	2761	ACGGCAGGCGCTGCGCACAGACAGTACACACCTCTCTTCCAGTCAATGTGTGGGCGCTG	2820
Db	2761	ACGGCAGGCGCTGCGCACAGACAGTACACACCTCTCTTCCAGTCAATGTGTGGGCGCTG	2820
Oy	2821	TAG 2823	
Db	2821	TAG 2823	
RESULT 2			
US-09-211-755-3			
Sequence 3, Application US/09211755			
GENERAL INFORMATION:			
APPLICANT: Jones, Kenneth A.			
APPLICANT: Laz, Thomas M.			
APPLICANT: Borowsky, Beth			
TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And			
TITLE OF INVENTION: Uses Thereof			
NUMBER OF SEQUENCES: 47			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Cooper & Dunham LLP			
STREET: 1185 Avenue of the Americas			
CITY: New York			
STATE: New York			
COUNTRY: U.S.A.			
ZIP: 10036			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211.755
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White Esq. John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 34002-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2823 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-09-211-755-3

Query Match 100.0% Score 2823: DB 42: Length 2823:
Best Local Similarity 100.0% Pred. No. 0:
Matches 2823: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1 ATGAGCTTCCCGCCGAGCTCCGGGAGCCCGCCGCGCCGCGCCGCGCCGCGCCGCG 60
DB 1 ATGAGCTTCCCGCCGAGCTCCGGGAGCCCGCCGCGCCGCGCCGCGCCGCGCCGCG 60
QY 61 CGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 CGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 TGGAGCGGG 180
DB 121 TGGAGCGGG 180
QY 181 ATGCGGCTCCAGCAAGAGGTGGCCAAAGGAGCATCGGGGGGGGGGGGGGGGGGGGG 240
DB 181 ATGCGGCTCCAGCAAGAGGTGGCCAAAGGAGCATCGGGGGGGGGGGGGGGGGGGGG 240
QY 241 GAGGTAGCCATGAGAGATCCGCAAGAGATCCGCGGGGGGGGGGGGGGGGGGGGGGG 300
DB 241 GAGGTAGCCATGAGAGATCCGCAAGAGATCCGCGGGGGGGGGGGGGGGGGGGGGGG 300
QY 301 CGACTATGACACCGAGTGTGACAAATGCAAAAGGAGCTGAAAGCTTTATGACGCAATA 360
DB 301 CGACTATGACACCGAGTGTGACAAATGCAAAAGGAGCTGAAAGCTTTATGACGCAATA 360
QY 361 AAGTATGGGCGCAACCATTTGATGTTTGGAGGCGTGTGCGAGTGTGACATCTATT 420
DB 361 AAGTATGGGCGCAACCATTTGATGTTTGGAGGCGTGTGCGAGTGTGACATCTATT 420
QY 421 ATGGCGGAGTCCCTCAAGGCTGGAATCTGGTGAAGCTTTCTTCCGCGGACAGGCT 480
DB 421 ATGGCGGAGTCCCTCAAGGCTGGAATCTGGTGAAGCTTTCTTCCGCGGACAGGCT 480
QY 481 GTTCTTGGGATTAAGAAAGTATCCGATTTCTTCGGAAGCGGTGCGGTGACAAAGCG 540
DB 481 GTTCTTGGGATTAAGAAAGTATCCGATTTCTTCGGAAGCGGTGCGGTGACAAAGCG 540
QY 541 GTGAGCCCGCCATCTGTAAGCTCTGAAGACATTCGCGTGGGCGGCGGTGAGGAGCAAC 600
DB 541 GTGAGCCCGCCATCTGTAAGCTCTGTAAGACATTCGCGTGGGCGGCGGTGAGGAGCAAC 600
QY 601 ACGGAGAGCTGAGCGCTTCTCCAGAGTGAAGAAATGACTGAGTGGGCTTGTATGGG 660
DB 601 ACGGAGAGCTGAGCGCTTCTCCAGAGTGAAGAAATGACTGAGTGGGCTTGTATGGG 660
QY 661 GAAGATTTGAGATCTCAGACAGAGAGTTTCTCCATGATCTCCCTCAGCAGCGTCAAA 720
DB 661 GAAGATTTGAGATCTCAGACAGAGAGTTTCTCCATGATCTCCCTCAGCAGCGTCAAA 720

DB 661 GAAGATTTGAGATCTCAGACAGAGAGTTTCTCCATGATCTCCCTCAGCAGCGTCAAA 720
QY 721 AAGCTCAAGGGAATGACGCGGATCATCTCTGGCCAGTTGACAGAAATATGAGGAGA 780
DB 721 AAGCTCAAGGGAATGACGCGGATCATCTCTGGCCAGTTGACAGAAATATGAGGAGA 780
QY 761 AAATCTTCTGTTGCTGCTTCCAGAGAGCATGTTGGCAGCAAGTACCGATGATCATC 840
DB 761 AAATCTTCTGTTGCTGCTTCCAGAGAGCATGTTGGCAGCAAGTACCGATGATCATC 840
QY 841 CCGGATGATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 CCGGATGATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 TGGCTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 TGGCTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 CTGAGCTTCAAGCAAAATCAAGACATCTCAGGGAAGACTCCACAGCATGTAAGAGAG 1020
DB 961 CTGAGCTTCAAGCAAAATCAAGACATCTCAGGGAAGACTCCACAGCATGTAAGAGAG 1020
QY 1021 TACAAGAGCAAAAGTTCAGGCGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1080
DB 1021 TACAAGAGCAAAAGTTCAGGCGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1080
QY 1081 ATCTGGGTCAATCGCCAAAGACCTTACAGAGGCGCATGAGACATCTGCTACATGAG 1140
DB 1081 ATCTGGGTCAATCGCCAAAGACCTTACAGAGGCGCATGAGACATCTGCTACATGAG 1140
QY 1141 CACAGGAGATCCAGAGACTTCAATACAGACACAGAGCTGGGCAAAATCAATCTCAAT 1200
DB 1141 CACAGGAGATCCAGAGACTTCAATACAGACACAGAGCTGGGCAAAATCAATCTCAAT 1200
QY 1201 GCAATGAAGAGACCAATCTTCCGGGGTCAAGGGTCAAGTGGTTCGGAAGGGGAG 1260
DB 1201 GCAATGAAGAGACCAATCTTCCGGGGTCAAGGGTCAAGTGGTTCGGAAGGGGAG 1260
QY 1261 AAGATGGGAACATTAATTTACTCAATTTCAAGACAGAGAGTGAAGTGGCGAA 1320
DB 1261 AAGATGGGAACATTAATTTACTCAATTTCAAGACAGAGAGTGAAGTGGCGAA 1320
QY 1321 TACAAGGAGGAGTGAACACATGAGATCATGACATCAATCAATCAATCAATCAATCA 1380
DB 1321 TACAAGGAGGAGTGAACACATGAGATCATGACATCAATCAATCAATCAATCAATCA 1380
QY 1381 GAGCCACCCAAAGACAAAGACATCTTGGAGAGCTTGGGAAGTCTGCTTCCACTG 1440
DB 1381 GAGCCACCCAAAGACAAAGACATCTTGGAGAGCTTGGGAAGTCTGCTTCCACTG 1440
QY 1441 TATAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 TATAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 TTCAAAATCAAGAAAGGAGAAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
DB 1501 TTCAAAATCAAGAAAGGAGAAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
QY 1561 CTGATCATCTGAGAGAAATGCTGCTATGATCATCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 1561 CTGATCATCTGAGAGAAATGCTGCTATGATCATCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 TCCCTGCTGAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1680
DB 1621 TCCCTGCTGAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1680
QY 1681 GTGGGCTACACACTGCTTGGGGCATGTTGCAAGACCTGAGAGGCTCATGCCATC 1740
DB 1681 GTGGGCTACACACTGCTTGGGGCATGTTGCAAGACCTGAGAGGCTCATGCCATC 1740
QY 1741 TTCAAAATGTAAGATGAAGAAAGATCATCAAGAGCTGCTGCTGCTGCTGCTGCTG 1800
DB 1741 TTCAAAATGTAAGATGAAGAAAGATCATCAAGAGCTGCTGCTGCTGCTGCTGCTG 1800

OY	361	AAAGTATGGGCGAACAACATTTGATGGATGTTGGAGGCGGTGTGCGTGTCAACATTAAT	420
Db	361	AAAGTATGGGCGTGAACCACTTTGATGGATGTTGGAGGCGGTGTGCGTGTCAACATTAAT	420
OY	421	ATCGCGGAGTCCCTCCAAAGGCTGGAAATCTGTGACAGCTTTCTTGGCCGACACAGCGCT	480
Db	421	ATCCCGGAGTCCCTCCAAAGGCTGGAAATCTGTGACAGCTTTCTTGGCCGACACAGCGCT	480
OY	481	GTTCTGTGGGATTAAGAGAGTACCCGATTTTCTCCGAGCGTGCCTGCACAGACGCG	540
Db	481	GTTCTGTGGGATTAAGAGAGTACCCGATTTTCTCCGAGCGTGCCTGCACAGACGCG	540
OY	541	GTGAACCCCGCCATCCTGAAGCTCTGAAACACTTCCGCTGGCGCGGTGTGGGACACTC	600
Db	541	GTGAACCCCGCCATCCTGAAGCTCTGAAAGCACTTCCGCTGGCGCGGTGTGGGACACTC	600
OY	601	ACGAGAGACGTCAGACGCTCTCTCCGAGGTAGAGAAAGCACTCACTGGGATTTGTATGG	660
Db	601	ACGAGAGACGTCAGACGCTCTCTCCGAGGTAGAGAAAGCACTCACTGGGATTTGTATGG	660
OY	661	GAAATATATGATCTCAGACACAGAGATTTCTCAATGATCCTGCACACAGCGTCAAA	720
Db	661	GAAATATATGATCTCAGACACAGAGATTTCTCAATGATCCTGCACACAGCGTCAAA	720
OY	721	AAGTCAAGGGGAATGACGTGGGATCATCCTTGGGCATTTGACACAAATATGSCACAA	780
Db	721	AAGTCAAGGGGAATGACGTGGGATCATCCTTGGGCATTTGACACAAATATGSCACAA	780
OY	781	AAAGTCTTTGTGTGTGCTTCCAGAGAGAGCATGTTTGGCAGCAAGTACCAGTGGATCATC	840
Db	781	AAAGTCTTTGTGTGTGCTTCCAGAGAGAGCATGTTTGGCAGCAAGTACCAGTGGATCATC	840
OY	841	CCGGAGTGTACGAG	900
Db	841	CCGGAGTGTACGAG	900
OY	901	TGCTGTGGGAG	960
Db	901	TGCTGTGGGAG	960
OY	961	CTGAGCTCCAAACAAATCAAGAGCACTCTCAGGAGAACTCCACAGCACTATGAAAGAGAG	1020
Db	961	CTGAGCTCCAAACAAATCAAGAGCACTCTCAGGAGAACTCCACAGCACTATGAAAGAGAG	1020
OY	1021	TACAAACAGCAACGTTAGGCGTGTGGGCGCCAGCAATCTGATGAGCTTACAGATGGG	1080
Db	1021	TACAAACAGCAACGTTAGGCGTGTGGGCGCCAGCAATCTGATGAGCTTACAGATGGG	1080
OY	1081	ATCTGGGTCATCGCAG	1140
Db	1081	ATCTGGGTCATCGCAG	1140
OY	1141	CACCAAGGAGATCCAGGAGCTCACTACAGAGACCAAGAGCTGGGCAAAATCATCTCAAT	1200
Db	1141	CACCAAGGAGATCCAGGAGCTCACTACAGAGACCAAGAGCTGGGCAAAATCATCTCAAT	1200
OY	1201	GCCATGAGACGAGCAACTTCTTCGAGGAGTACGCGGTCAAGTGTGTCTCGGAAACGGGAG	1260
Db	1201	GCCATGAGACGAGCAACTTCTTCGAGGAGTACGCGGTCAAGTGTGTCTCGGAAACGGGAG	1260
OY	1261	AGAAATGGGAACCATTAATTTACTCAATTTCAAGACAGAGAGAGAGAGAGAGAGAGAGAG	1320
Db	1261	AGAAATGGGAACCATTAATTTACTCAATTTCAAGACAGAGAGAGAGAGAGAGAGAGAGAG	1320
OY	1321	TACAAACGCGGTGTGACACACTGTGAGATCATCAATGACACCATTAAGGTTCCAGGGGTC	1380
Db	1321	TACAAACGCGGTGTGACACACTGTGAGATCATCAATGACACCATTAAGGTTCCAGGGGTC	1380
OY	1381	GAGGACCCCAAGGACAGAGACATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1440
Db	1381	GAGGACCCCAAGGACAGAGACATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1440

QY	1441	TATGATCCCTGTCGCGCTGTCACATCTCGGATGATCATGGCAGGCGCTTCCTTC	1500
QY	1441	TATGATCCCTGTCGCGCTGTCACATCTCGGATGATCATGGCAGGCGCTTCCTTC	1500
Db	1441	TATGATCCCTGTCGCGCTGTCACATCTCGGATGATCATGGCAGGCGCTTCCTTC	1500
QY	1501	TTCAACATCAAGAACCGGAACCAAAAGCTGATTAAATGATCAAGCCCTCATGTAACAC	1560
Db	1501	TTCAACATCAAGAACCGGAACCAAAAGCTGATTAAATGATCAAGCCCTCATGTAACAC	1560
QY	1561	CTCATCATCCCTGGGAGAAAGCTGTCCTTATGATCATCTTCCTTTGGGCTCGATGG	1620
Db	1561	CTCATCATCCCTGGGAGAAAGCTGTCCTTATGATCATCTTCCTTTGGGCTCGATGG	1620
QY	1621	TCCTTGTCTCAGAAAAGACCTTTGAACACTCTGACAGGTCCGAACTGATTCAC	1680
Db	1621	TCCTTGTCTCAGAAAAGACCTTTGAACACTCTGACAGGTCCGAACTGATTCAC	1680
QY	1681	GTGGGCTACACAACTGCGCTTTGGGGCCATGTTGGAAGAGCTGGAGGTCATGCCATC	1740
Db	1681	GTGGGCTACACAACTGCGCTTTGGGGCCATGTTGGAAGAGCTGGAGGTCATGCCATC	1740
QY	1741	TTCAAAATGTGAAGATGAAGAAGATCATCAAGACAGACGCTCTGTGATTGTG	1800
Db	1741	TTCAAAATGTGAAGATGAAGAAGATCATCAAGACAGACGCTCTGTGATTGTG	1800
QY	1801	GGGGGCACTGCTGTCATCGACTGTGCTCATCTGATCTGTTGGCAAGCTGTGGACCCCTG	1860
Db	1801	GGGGGCACTGCTGTCATCGACTGTGCTCATCTGATCTGTTGGCAAGCTGTGGACCCCTG	1860
QY	1861	CGAGAGACATGAAGAGGTACAGCATGAGAGCCGGACCCAGCAGGCGGAGACATCTCCATC	1920
Db	1861	CGAGAGACATGAAGAGGTACAGCATGAGAGCCGGACCCAGCAGGCGGAGACATCTCCATC	1920
QY	1921	CGCCCATTTGCTGGAACACTGCGAAGAACACCCACATGACCATTGCGTTGGCATGTCTAC	1980
Db	1921	CGCCCATTTGCTGGAACACTGCGAAGAACACCCACATGACCATTGCGTTGGCATGTCTAC	1980
QY	1981	GCCCTACAGGGGGGCGCTCATGATCGGTTGTTCTTGGCATGGGAACCCGCAATGTG	2040
Db	1981	GCCCTACAGGGGGGCGCTCATGATCGGTTGTTCTTGGCATGGGAACCCGCAATGTG	2040
QY	2041	AGCATCCCTGCCCTCAACGACACAGACAGTACATCGGATGAGTGTGTACAAATGTGGGATC	2100
Db	2041	AGCATCCCTGCCCTCAACGACACAGACAGTACATCGGATGAGTGTGTACAAATGTGGGATC	2100
QY	2101	ATGTCACATCATCGGGGCGTGTCTCTCTCTCGAGCGGACGACACCCAAAGCTGCAATTC	2160
Db	2101	ATGTCACATCATCGGGGCGTGTCTCTCTCTCGAGCGGACGACACCCAAAGCTGCAATTC	2160
QY	2161	TGCATGCTGGCCCTGGTTCATCATCTTCTGACAGCACCATCTCTCTGCTGGTGTGTG	2220
Db	2161	TGCATGCTGGCCCTGGTTCATCATCTTCTGACAGCACCATCTCTCTGCTGGTGTGTG	2220
QY	2221	CCAAAGCTCATTTACTCTGAGAGCAAAACCTGAGCGGCACTCAACAAAGGGGTTCCAG	2280
Db	2221	CCAAAGCTCATTTACTCTGAGAGCAAAACCTGAGCGGCACTCAACAAAGGGGTTCCAG	2280
QY	2281	TTCAACAGAAACAGAGAAGAAGATTGGAAGACCTCCACTTCAAGTACACAGCGTGAAC	2340
Db	2281	TTCAACAGAAACAGAGAAGAAGATTGGAAGACCTCCACTTCAAGTACACAGCGTGAAC	2340
QY	2341	CAGCGAGACAGTACAGCCCTGAGAGGAGCTGCAATCAGAAACACACCGCTTCGAATTGAG	2400
Db	2341	CAGCGAGACAGTACAGCCCTGAGAGGAGCTGCAATCAGAAACACACCGCTTCGAATTGAG	2400
QY	2401	ATCAACAGAGCTGGACAAAGACTTGGAAAGATGCCATGACGTAACAGACACACACAGAG	2460
Db	2401	ATCAACAGAGCTGGACAAAGACTTGGAAAGATGCCATGACGTAACAGACACACACAGAG	2460
QY	2461	AAGACCAATATACATCAAAAGATCACTACCAAGAGCTCAAGCATCTCTCAGCTTGGGC	2520
Db	2461	AAGACCAATATACATCAAAAGATCACTACCAAGAGCTCAAGCATCTCTCAGCTTGGGC	2520
QY	2521	AACCTTCAAGAGACACAGATGAGGAAAGGCCATTCTTAAAAATTCACCTGATCAAAAC	2580

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Db 2521 AACTTCACAGAGACGACAGATGGAGAAAGCCATTCTTAAAAATCACCCTGCATTAAC 2580
QY 2581 CCCAGCTCCAGTGGAAACAGACAGAGCCCTTCAGAACATGCAAGAGCCCATAGAGAC 2640
Db 2581 CCCAGCTCCAGTGGAAACAGACAGAGCCCTTCAGAACATGCAAGAGCCCATAGAGAC 2640
QY 2641 ATCAACTCCCGGAGACACATCCAGGCGCGGCTGTGCTTCAGACTCCCATCTTACAC 2700
Db 2641 ATCAACTCCCGGAGACACATCCAGGCGCGGCTGTGCTTCAGACTCCCATCTTACAC 2700
QY 2701 GCTTACTCCATCCATCGAGAGCGGTGATGCGACGTCGTCAGCCCTGTGTAGCCCT 2760
Db 2701 GCTTACTCCATCCATCGAGAGCGGTGATGCGACGTCGTCAGCCCTGTGTAGCCCT 2760
QY 2761 ACCGCAAGCCCTCGCCACAGACAGACGTCACCCCTTCCTCGAGTCATGCTCGGCGCTG 2820
Db 2761 ACCGCAAGCCCTCGCCACAGACAGACGTCACCCCTTCCTCGAGTCATGCTCGGCGCTG 2820
QY 2821 TAG 2823
Db 2821 TAG 2823
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RESULT 4

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PCT-US99-11869-2
; Sequence 2, Application PC/TUS9911869
; GENERAL INFORMATION:
; APPLICANT: United States of America, represented by Sec. HHS
; APPLICANT: Clark, Janet
; APPLICANT: Bonner, Tom I.
; TITLE OF INVENTION: Mammalian gb2 GABAB Receptors
; FILE REFERENCE: 65879
; CURRENT APPLICATION NUMBER: PCT/US99/11869
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,274
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 5459
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PCT-US99-11869-2
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Query Match 99.8%; Score 2816.2; DB 1; Length 5459;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2818; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 1 ATGCTTCCCGCGAGCTCCGGGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db 151 atgcttcccgcgagctccgggcgagcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 210
QY 61 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 211 cgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 270
QY 121 TGGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 180
Db 271 tggagcgggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgctc 330
QY 181 ATGCCGCTCCACCAAGAGAGTGCCCAAGGGCAGCATCGGGCGCGCGCTGCTCCGCGCTG 240
Db 331 atgccgctccaccaaggagggtggccaaggcagcatcgcgcgcgctgctcccgcgctg 390
QY 241 GAGCTAGCATGAGACATCGCAAGAGTCACTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTG 300
Db 391 gagctagcatgagacatcgcaaggagtcaactcctgcgcgcgctgctgctgctgctgctg 450
QY 301 CGACTCTATGACACCGAGCTGTGACATGCAAGGACTGAAGGCTTTCTATGACGCAATA 360
Db 451 cgactctatgacaccgagtgtagacaatgcaaggagctgaagaccttctatgagcaata 510
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QY 361 AAGTATGCGCCGAACCATTTGATGTGTTTGGAGCGCTGTGCTGCTGCTGCTGCTGCTGCT 420
Db 511 aagtatgcgccgaacccatttgaatgtgttggagcgctgtgctgctgctgctgctgctgct 570
QY 421 ATGGCGAGTCCCTCCAGGCTGGATCTGTGTCAGACTTTCCTTGGCGCGCACACGCT 480
Db 571 atggcgagtccctccaggcttggaaatctgtgtgagcttctcctgcgcgcacacgctt 630
QY 481 GTTCTTCGATTAAGAAAGATACCCGTAATTTCTTCGAGCGGTGCGACAGCAACGCG 540
Db 631 gtcttcgagataagaagaatcccgatcttctccgagcggtgcgcaagaacgcg 690
QY 541 GTAAACCCCGCATCTCTGAAGCTCTGAAGACATTCGCTGGCGCGGTGCGACACTC 600
Db 691 gtgaaccccgcatctctgaagctctcgaagcacttcgctgcggtgtgtggcaacac 750
QY 601 ACCGAGACTGACAGGCTTCTCCGAGGTGAGGATGAGTACCTGACTGTGGGTTCTGATGG 660
Db 751 accgagactgacagggcttctccgaggtgaggaatgacctgactgtgtgtatggtg 810
QY 661 GAAGATATTAGATCTCAGACAGAGAGTTCTCCATGATCCCTGCACAGCGCAAA 720
Db 811 gaagatatgagatctcagacacagagagttctccaatgacctgcgcacgagcaaa 870
QY 721 AAGCTCAAGGGAATGACGTGCGGATCATCTTGGCAGTTTGACCAATATGACGCA 780
Db 871 aagctcaagggaatgacgtgcgcatccttgscagcttgacacagatatgtgcagga 930
QY 781 AAGTCTTCTGTTGTGCTTCCAGGAGACATGTTTGGACAGCAAGTACAGTGCATC 840
Db 931 aagctctctgtgtgtccttcgagagacatgttgcagcaagttacagtgatcacc 990
QY 841 CCGAGATGTACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 991 ccgagatgtacagcgctgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1050
QY 901 TGCCTGCGCAGAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 1051 tgcctgcgcagaaagctcctgtgcctgtgcctgtgcctgtgcctgtgcctgtgcctgtgcct 1110
QY 961 CTGAGCTCCCAAAATCAAGACCATCTCAGGGAAGACTCCACAGCATGTAAGAAGAG 1020
Db 1111 ctgagctcccaaaatacaagaccatctcagggaaagactccacagcagtttgaagagag 1170
QY 1021 TACAACAGCAAAAGCTTCAGAGCGGTGCGGCGCAGAGTTTCATGGGATGACCCATGAG 1080
Db 1171 tacaacagcaaaaagcttcagagcggtgcgcgcaagttccatggtgacgctcagatggg 1230
QY 1081 ATCTGGGTATCGCAAGACCTTACAGAGGCGCATGAGACACTGCTATGCCAGTAGCAG 1140
Db 1231 atctgggtatcgcaagaccttacagagcgcatgagagacactgacgtagcgagcg 1290
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QY 1201 GCCATGAAGAGACCAACTTCTCGGGGTCTACGGGTCAGTGTGTGTCGGGAAGGGGAG 1260
Db 1351 gccatgaagagaccaaacttctcggggtcagcggtcaggtgtgtcgcggaaggag 1410
QY 1261 AGAATGGGAACCAATTAATTTACTCAATTTCAAGACAGCAGAGAGTGAAGTCCGCGCA 1320
Db 1411 agaattgggaaccaaatttactcaatttcaagacagagagaggtgagagtcgagaa 1470
QY 1321 TACAAGCGGTGGCTACACACTGGGATCATCATGACACCATTAAGTTCCAGGGGCTC 1380
Db 1471 tacaagcggtggctacacactgggatacatcatgacacataaagtttccaagggctc 1530
QY 1381 GAGCCACCCCAAGGACAAGACCATCATTTCTGAGCAGCTTCGGAAGATCTCGCTTCCACTG 1440
Db 1531 gagccaccccaaggacaagacatcatcttgcgagcagcttcggaagatctcgcttccactg 1590
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QY 1441 TATAGATCTCTGCGCTCTCATCATCTCGGATGATCATGCGCAGCGCTTCTCTTC 1500
DB 1591 tatagatctctgCGCTctcaCATctccgcgcgtcatctgcaagcgcctctcttc 1650
QY 1501 TTCACATCAAGAACCGGAAACCAAGTGTATAGATGTCAAGCCCTACATGAACAC 1560
DB 1651 TTCACATCAAGAACCGGAAACCAAGTGTATAGATGTCAAGCCCTACATGAACAC 1710
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DB 1711 ctcatactcttggaggaaTgtctcctaTgatactctctctcttggctcgaaggg 1770
QY 1621 TCTCTGTCTAGAAAAGACTTTGAACACTCTGCACGGTCCGGACTGGATTCTCAC 1680
DB 1771 tctctgtctcaaaaagaccttTgaacactctgcacgcgtccgaactgtatctcacc 1830
QY 1681 GTGGGCTACACAATCGCTTTGGGGCCATGTTTGCAAGACTGGAGGGTCCATGCCATC 1740
DB 1831 gtgggctacacaactgccttTggggccatgtttgcaaaagacctggaaggtccatgtccatc 1890
QY 1741 TTCAAAATGTGAAGATGAAGAAGATCATCAAGACAGACGCTGCTGTGATTGTG 1800
DB 1891 ttcaaaatgtgaagaTgaagaagaagatcatcaaaagaccgaagctgtctgtgattgtg 1950
QY 1801 GGGGGCATGCTGCTCATCGACCTGTGCATCTGATCTGTTGGCAGGCTGTGGACCCCTG 1860
DB 1951 gggggcatgctgctcatcgactgtgcactgtcatctgtctgtgcagctgtgagaccctgt 2010
QY 1861 CGAGAGACGTAGAGAGTACAGCATGGAGCCGGACCCAGACGGCCGGGACATCTCCATC 1920
DB 2011 cgagagacgtagagagTacagcatgagccgagccagcagcgggaacatctccatc 2070
QY 1921 CCCCCATTGCTGGAACACTGCGAAAAACCCACATGACCATCTGCTTGGCATTTGTAC 1980
DB 2071 cggccattgtgaaacactgcgaaaaacacccacatgacatctgtctgtgattctaac 2130
QY 1981 GCCTCAGAGGGCTCCTCATCTGCTATTCGGTGTTCCTTGGCATGGGAAACCCGCAATGTG 2040
DB 2131 gctctcaaggggtcctcatgtatctgtgttcttctgtgcattggaacccgcgaatgtg 2190
QY 2041 AGCATTCCTCGCCCTCAACACAGCAAGTACATCGGATGAGTGTACAATGTGGGGATC 2100
DB 2191 agcatctccgcctcaacacagcagcatcatcgcatgagtgtaaatgtgaggatc 2250
QY 2101 AATGTCATCATGGGGCTGCTGTCTCTCTCTGACGCGTGAACCCCAAGCTGAGTTC 2160
DB 2251 aatgtcatcatggggctgtctctctctctcctgcagcgtgaccagcccaagctgagttc 2310
QY 2161 TGCATCTGGCCCTGGTCTCATCTTCTTGACAGCACCATCATCTCTGCTGGTGTGTG 2220
DB 2311 tgcattgtggccctggctcatctctctgcagcacatcatctctgcctgtgtgtgtg 2370
QY 2221 CCAAAAGCTATTAATCTGAGCAAAACCTGACGACGCACTCAACAAGAGGGTTCAG 2280
DB 2371 ccaaaagctatatactctgagcaaaacctgagcagccaacgaagaaggggttcag 2430
QY 2281 TTCACACAGAACCCAGAGAAAGATTTGGAAGACTCCACTTCACTACACAGCTGAA 2340
DB 2431 ttcacacagaaacagaaagaagaattcgaagacctccactctgtaaccagcgtgaaac 2490
QY 2341 CAGGGCAGCAGCTCAGCGCTGAGGAGTGCAGTCAGAAAACACCGCTTGGATGAAG 2400
DB 2491 caggcagcagctcagccttggaggactgcagtcagaaacacacgccttcgaatgaag 2550
QY 2401 ATCAGCAGACTGGACAAACTTGAAGAAGTCAACATGCACTACAGACACACAGAG 2460
DB 2551 atcagcagactggacaAAacttgaagaagtcacacatgcagctcaagaacacaccagag 2610
QY 2461 AAGACCATATCATCAAAAGAAATCACTACAGAGCTCAAGACATGCTCAGTTGGGC 2520
DB 2611 aagacacatactcaaaagaatactactcaagagctcaagaatactctcagcttgggc 2670
QY 2521 AACTTCACAGAGACAGATGAGGAAAGGCCAATTCTAAAAAATCACCTCGATCAAAAC 2580

DB 2671 aacttcagagagcagagatggaaagggccattctaaataacactcgatcaaaac 2730
QY 2581 CCCAGCTCAGTGGAAACGAGCAGAGCCCTCAAGAACATGCAAGACCCCATAGAAGAC 2640
DB 2731 cccagctcagtggaacacagacagagccctcaagaacatgcaagaccccatagaagac 2790
QY 2641 ATCAACTCCCGGAGCACAATCCAGGCGCGCTGTGCTTCCAGCTCCCATCTTCAACAC 2700
DB 2791 atcaactcccgagagacatccagcgcgctgtctcagctcccatctctcaaccac 2850
QY 2701 GCCTACTCCCATCATCGAGAGCGTGGATGCGACGTGCTAGCCCTGTCTCAGCCCT 2760
DB 2851 gcctactcccatcatcagcagagcttgagatgccaagctgcgtcagccctgttcagccct 2910
QY 2761 ACCGCGAGCGCTGGCAGACAGACGATCACACCTCTCTCCAGTATGGTCTCGGCGCTG 2820
DB 2911 accgcgagcgcctggcacagacagtlacacacctctctccagatcgtctcgggctgt 2970
QY 2821 TAG 2823
DB 2971 tag 2973

RESULT 5
PCT-US98-22033-3
; Sequence 3, Application PC/TUS9822033
; GENERAL INFORMATION:
; APPLICANT: SYNAPTRIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING A GABABR2 POLYPEPTIDE AND USES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/22033
; FILING DATE: 16-OCT-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28, 678
; REFERENCE/DOCKET NUMBER: 1795/54002-B-PCT/JPW/ADM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2652 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: NO
; ANTI-SENSE: NO
PCT-US98-22033-3

Query Match 93.9%; Score 2650.4; DB 1; Length 2652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 172 ATGGGCTCATGCGCGCTCACCAAGAGGTGGCCAAAGGCGACGATGGGCGGCGTCTC 231
|||||

Db 1 ATGGGCTCATGCGGCTCACCAGAGAGTGCCAGAGGCGCAGCATCGGGCGCGCTGCTC 60
Qy 233 CCGGCGGAGGAGCGATGAGCATGCGAGATCGGAGAGTCACTCTGGCGCCCTACTTC 291
Db 61 CCGGCGGAGGAGCGATGAGCATGCGAGATCGGAGAGTCACTCTGGCGCCCTACTTC 120
Qy 292 CTGACACTGCGACTCTATGACACCGAGTGTGACATGCAAGGAGTGAAGCCTCTAT 351
Db 121 CTGACACTGCGACTCTATGACACCGAGTGTGACATGCAAGGAGTGAAGCCTCTAT 180
Qy 352 GACGGAATTAAGTATGGGCGGCAACATTTGATGTTGGAGGCGCTGTCCGCTGTC 411
Db 181 GACGGAATTAAGTATGGGCGGCAACATTTGATGTTGGAGGCGCTGTCCGCTGTC 240
Qy 412 ACATCTATTATCGGAGATCCCTCCAGGCTGGAATCTGTGAGCTTCTCTCCGCGC 471
Db 241 ACATCTATTATCGGAGATCCCTCCAGGCTGGAATCTGTGAGCTTCTCTCCGCGC 300
Qy 472 ACCAGCGCTCTTCTGGGAGTAAAGAAAGTACCCCTATTCTTCCGAGGCGCTGCA 531
Db 301 ACCAGCGCTCTTCTGGGAGTAAAGAAAGTACCCCTATTCTTCCGAGGCGCTGCA 360
Qy 532 GACAACGCGGTGAACCCCGCATCTGAAGCTCTGAAGCACTTCGCTGCGCGCTGTG 591
Db 361 GACAACGCGGTGAACCCCGCATCTGAAGCTCTGAAGCACTTCGCTGCGCGCTGTG 420
Qy 592 GGCACACTCAGCGAGAGAGTGCAGCGCTTCTCCGAGGTGAGAAATGACTGATGGGCT 651
Db 421 GGCACACTCAGCGAGAGAGTGCAGCGCTTCTCCGAGGTGAGAAATGACTGATGGGCT 480
Qy 652 CTGTATGGGGAAGATTAATGATCTCAGACACAGAGATTTCTCAATGATCCCTGACC 711
Db 481 CTGTATGGGGAAGATTAATGATCTCAGACACAGAGATTTCTCAATGATCCCTGACC 540
Qy 712 AGCGCAAAAAGCTCAAGGGAATGAGTGGGATCATCTTGGCGCAATTTGACCAAGAT 771
Db 541 AGCGCAAAAAGCTCAAGGGAATGAGTGGGATCATCTTGGCGCAATTTGACCAAGAT 600
Qy 772 ATGGCAGCAAAAAGTCTTGTGTGTGCTTCGAGAGAGCATGTTTGGCAGCAAGTACAG 831
Db 601 ATGGCAGCAAAAAGTCTTGTGTGTGCTTCGAGAGAGCATGTTTGGCAGCAAGTACAG 660
Qy 832 TGATCATCCCGGATGTGATGAGCTGCGGTGGGAGAGAGTGAAGTGAAGGCGCAT 891
Db 661 TGATCATCCCGGATGTGATGAGCTGCGGTGGGAGAGAGTGAAGTGAAGGCGCAT 720
Qy 892 TCCTCAGCGCTGCTGCGAGAGAGCTCTGCTGCTGCAATGGAAGTTACATCGAGTGAAC 951
Db 721 TCCTCAGCGCTGCTGCGAGAGAGCTCTGCTGCTGCAATGGAAGTTACATCGAGTGAAC 780
Qy 952 TTTGAGCCCGCTGAGTCCCAAAACAATCAAGCATCTCAGGGAAGAGTCCACAGCATAT 1011
Db 781 TTTGAGCCCGCTGAGTCCCAAAACAATCAAGCATCTCAGGGAAGAGTCCACAGCATAT 840
Qy 1012 GAAAGAGATACAGAGCAAAAGTTCAGGCGTGGGCGCCAGCAAGTTCATGGGTAGGCC 1071
Db 841 GAAAGAGATACAGAGCAAAAGTTCAGGCGTGGGCGCCAGCAAGTTCATGGGTAGGCC 900
Qy 1072 TACGATGGGATGTGGGTATGCGCCAAAGCCTTACAGAGGCGCATGGAATCTGATGCC 1131
Db 901 TACGATGGGATGTGGGTATGCGCCAAAGCCTTACAGAGGCGCATGGAATCTGATGCC 960
Qy 1132 AGTAGAGGACACAGCGATCCAGGATCTCAACTACAGACACAGCGTGGGCAAAATC 1191
Db 961 AGTAGAGGACACAGCGATCCAGGATCTCAACTACAGACACAGCGTGGGCAAAATC 1020
Qy 1192 ATCTCTAAATGCCATGAAGAGACCACTTCTGGGGGTCAAGGTTGATGTTCCGG 1251
Db 1021 ATCTCTAAATGCCATGAAGAGACCACTTCTGGGGGTCAAGGTTGATGTTCCGG 1080
Qy 1252 AACGGGAGAGAGATGGAGACCTTAATTTACTCAATTTCAAGACAGCAGAGAGTGAAG 1311
Db 1081 AACGGGAGAGAGATGGAGACCTTAATTTACTCAATTTCAAGACAGCAGAGAGTGAAG 1140

Qy 1312 GTGCGGAAATACAAAGCGGTGGTGTGACACACTGAGATCATCATGACACCATTAAGTTC 1371
Db 1141 GTGCGGAAATACAAAGCGGTGGTGTGACACACTGAGATCATCATGACACCATTAAGTTC 1200
Qy 1372 CAGGGGTCCGAGCCACCCAGAGACAGACATCATCTTGAGAGCTTGGGAATCTCG 1431
Db 1201 CAGGGGTCCGAGCCACCCAGAGACAGACATCATCTTGAGAGCTTGGGAATCTCG 1260
Qy 1432 CTTCACATGTATAGATCTGTCCGCTCTCACATCTCTGGCATGTATCATGAGCAGCGC 1491
Db 1261 CTTCACATGTATAGATCTGTCCGCTCTCACATCTCTGGCATGTATCATGAGCAGCGC 1320
Qy 1492 TTCTCTTCTTCAATCATCAGAACCGGACAAAAGCTGATTAAGATGTCAGACCCCTAC 1551
Db 1321 TTCTCTTCTTCAATCATCAGAACCGGACAAAAGCTGATTAAGATGTCAGACCCCTAC 1380
Qy 1552 ATGAACAACCTCATCATCTGAGAGAAAGTGTGCTATGATCATCTCTCTCTTGGC 1611
Db 1381 ATGAACAACCTCATCATCTGAGAGAAAGTGTGCTATGATCATCTCTCTCTTGGC 1440
Qy 1612 CTGATGGGTCTCTGCTCAGAAAAAGCCTTGAACACTGTGACAGGTCCGGACCTGG 1671
Db 1441 CTGATGGGTCTCTGCTCAGAAAAAGCCTTGAACACTGTGACAGGTCCGGACCTGG 1500
Qy 1672 ATTTCACCGTGGGTACACAAGTGCCTTGGGGCCATGTTTGAAGAGACTGAGAGGTC 1731
Db 1501 ATTTCACCGTGGGTACACAAGTGCCTTGGGGCCATGTTTGAAGAGACTGAGAGGTC 1560
Qy 1732 CATGCCATCTTCAAAATGTGAAGATGAAGAGATCATCAAGACCAAGACTGCTT 1791
Db 1561 CATGCCATCTTCAAAATGTGAAGATGAAGAGATCATCAAGACCAAGACTGCTT 1620
Qy 1792 GTGATGTGGGGGAGATCTGTGATGATGAGCTGTGATCTGATCTGTTGGCAGGCTGTG 1851
Db 1621 GTGATGTGGGGGAGATCTGTGATGATGAGCTGTGATCTGATCTGTTGGCAGGCTGTG 1680
Qy 1852 GACCCCTCGGAGACAGTGAAGAGTACAGCATGGAAGCCGAGACCGAGCGGGAC 1911
Db 1681 GACCCCTCGGAGACAGTGAAGAGTACAGCATGGAAGCCGAGACCGAGCGGGAC 1740
Qy 1912 ATCTCATCGGCGCATCTGCTGGAACACTGCGAAACACCCACATGACATCTGCTTGGC 1971
Db 1741 ATCTCATCGGCGCATCTGCTGGAACACTGCGAAACACCCACATGACATCTGCTTGGC 1800
Qy 1972 ATTGTACGCTTACAGAGGGGCTCTCATGCTATTCGTTGTTCTTGGCATGGAACC 2031
Db 1801 ATTGTACGCTTACAGAGGGGCTCTCTCATGCTATTCGTTGTTCTTGGCATGGAACC 1860
Qy 2032 CGCATGTGAGCATCCCTGCGCCTCAAGACAGCAAGTACATCGGCATGAGTGTACAT 2091
Db 1861 CGCATGTGAGCATCCCTGCGCCTCAAGACAGCAAGTACATCGGCATGAGTGTACAT 1920
Qy 2092 GTGGGATCATGTGATCATCGGGGCTGTGCTCTTCTGACGCGTGAACGCCAAT 2151
Db 1921 GTGGGATCATGTGATCATCGGGGCTGTGCTCTTCTGACGCGTGAACGCCAAT 1980
Qy 2152 GTGCAATTCGATGCTGCGCCTGATCATCTTCTGACAGACATCATCTCTGCTG 2211
Db 1981 GTGCAATTCGATGCTGCGCCTGATCATCTTCTGACAGACATCATCTCTGCTG 2040
Qy 2212 GTGTTGTGCCAAAGCTATTACTGTGAGCAAAACCTTGACGCGCATCAAGACAG 2271
Db 2041 GTGTTGTGCCAAAGCTATTACTGTGAGCAAAACCTTGACGCGCATCAAGACAG 2100
Qy 2272 CGGTTCCAGTTCACAGAGACAGAAAGAAAGTTGGAAGACCTCACTTGAAGTCAAC 2331
Db 2101 CGGTTCCAGTTCACAGAGACAGAAAGAAAGTTGGAAGACCTCACTTGAAGTCAAC 2160
Qy 2332 AGCGTGAACGAGCGAGCATGTCAGCGCTGAGAGAGTGAAGTGAAGAAACACGCGCTT 2391
Db 2161 AGCGTGAACGAGCGAGCATGTCAGCGCTGAGAGAGTGAAGTGAAGAAACACGCGCTT 2220

QY 2392 CGATGAGATCATCAGACCTGAGCAAGACTGTGAGAAAGTCCATCCAGCTACAGAC 2451
 Db 2221 CGATGAGATCATCAGACCTGAGCAAGACTGTGAGAAAGTCCATCCAGCTACAGAC 2280
 QY 2452 ACACCAAGAGAGACCATATCATCAAAAGATTCATCCAGAGCTCAACGACATCTTC 2511
 Db 2281 ACACCAAGAGAGACCATATCATCAAAAGATTCATCCAGAGCTCAACGACATCTTC 2340
 QY 2512 AGCTTGGGCACTTCCACAGAGACAGATGAGAGAAAGCCATTCTAAAAATACCTTC 2571
 Db 2341 AGCTTGGGCACTTCCACAGAGACAGATGAGAGAAAGCCATTCTAAAAATACCTTC 2400
 QY 2572 GATCAAAACCCCACTCTCACTGAGACAGAGAGCCCTCAAGAAATGCAAGACCCC 2631
 Db 2401 GATCAAAACCCCACTCTCACTGAGACAGAGAGCCCTCAAGAAATGCAAGACCCC 2460
 QY 2632 ATAGAAGACATCACTCCCGAGACAGATCAGAGCCGCTGCTCCAGATCCCATC 2691
 Db 2461 ATAGAAGACATCACTCCCGAGACAGATCAGAGCCGCTGCTCCAGATCCCATC 2520
 QY 2692 CTTCACACAGCTTACCTCCATCCATCGAGAGCGGTGAGTCCAGCTGAGCCCTGT 2751
 Db 2521 CTTCACACAGCTTACCTCCATCCATCGAGAGCGGTGAGTCCAGCTGAGCCCTGT 2580
 QY 2752 GTGAGCCCTACCGCCGCTCGCCACAGACAGATCAACCCCTCTCCAGATCAGTTC 2811
 Db 2581 GTGAGCCCTACCGCCGCTCGCCACAGACAGATCAACCCCTCTCCAGATCAGTTC 2640
 QY 2812 TGGGCGCTGTAG 2823
 Db 2641 TGGGCGCTGTAG 2652

RESULT 6

PCT-US98-22033A-3
 Sequence 3, Application PC/TUS9822033A

GENERAL INFORMATION:

APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
 TITLE OF INVENTION: DNA ENCODING A GABAR2 POLYPEPTIDE AND USES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.

ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US98/22033A
 FILING DATE: 16-OCT-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 1795/54002-B-PCT/JPM/ADM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 351-0525

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2652 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ANTI-SENSE: NO

PCT-US98-22033A-3

Query Match 93.9%; Score 2650.4; DB 1; Length 2652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 172 ATGGAGCTCATGCGGCTCATCAAGAGAGTGGCCAAAGGACAGATCGGGCGGGGCTTC 231
 Db 1 ATGGAGCTCATGCGGCTCATCAAGAGAGTGGCCAAAGGACAGATCGGGCGGGGCTTC 60
 QY 232 CCGCGCGTGAAGCTATGACATGAGCAGATCGGCAAGAGTACTCTCGCCCTACTTC 291
 Db 61 CCGCGCGTGAAGCTATGAGCAGATCGGCAAGAGTACTCTCGCCCTACTTC 120
 QY 292 CTGGACCTGGACCTCTATGACACCGAGTGTGACATGCAAAAGGAGCTGAAAGCTTAT 351
 Db 121 CTGGACCTGGACCTCTATGACACCGAGTGTGACATGCAAAAGGAGCTGAAAGCTTAT 180
 QY 352 GACGCAATAAAGTATGAGGCGGAACATTTGATGTGTGGAAGCGTCTGTCTGTC 411
 Db 181 GACGCAATAAAGTATGAGGCGGAACATTTGATGTGTGGAAGCGTCTGTCTGTC 240
 QY 412 ACATCTATATCGGGAGTCCCTCCAAAGCTGGAATCTGTGACAGCTTCTTGGCCGCC 471
 Db 241 ACATCTATATCGGGAGTCCCTCCAAAGCTGGAATCTGTGACAGCTTCTTGGCCGCC 300
 QY 472 ACCAGCCTGTCTTCTGGGATAGAAAGAAAGTACCCGTATTTCTTCCGAGCGTCTCA 531
 Db 301 ACCAGCCTGTCTTCTGGGATAGAAAGAAAGTACCCGTATTTCTTCCGAGCGTCTCA 360
 QY 532 GACAACGGGTGTAACCCCGCATCTGAAAGCTCTGAAAGCACTTCGCTGGCGGCTGTG 591
 Db 361 GACAACGGGTGTAACCCCGCATCTGAAAGCTCTGAAAGCACTTCGCTGGCGGCTGTG 420
 QY 592 GGCACATCTACAGAGAGAGCTGAGGCGCTTCTCCAGAGTGAAGATGACCTGAGGCTT 651
 Db 421 GGCACATCTACAGAGAGAGCTGAGGCGCTTCTCCAGAGTGAAGATGACCTGAGGCTT 480
 QY 652 CTGTATGGGAGATATATGATCTCAGACAGAGAGTTCCTCCATGATCCCTGCAC 711
 Db 481 CTGTATGGGAGATATATGATCTCAGACAGAGAGTTCCTCCATGATCCCTGCAC 540
 QY 712 AGCGCAAAAGCTCAAGGGGATGAGGAGTGGGATCATCTTGGCCAGTTGACCAAT 771
 Db 541 AGCGCAAAAGCTCAAGGGGATGAGGAGTGGGATCATCTTGGCCAGTTGACCAAT 600
 QY 772 ATGGCAGCAAAAGTCTTCTGTCTGCTTCAAGAGACATGTTGGCAGCAATACAG 831
 Db 601 ATGGCAGCAAAAGTCTTCTGTCTGCTTCAAGAGACATGTTGGCAGCAATACAG 660
 QY 832 TGGATCATCCCGGATGATGACAGGCTGCTGTGGTGGAGGAGGATGAGAGGCCAAT 891
 Db 661 TGGATCATCCCGGATGATGACAGGCTGCTGTGGTGGAGGAGGATGAGAGGCCAAT 720
 QY 892 TCCTCAGCTGCTGCGGAGAGAGCTCTGCTGCTGAGAGGATGAGAGGATGAGAGGAC 951
 Db 721 TCCTCAGCTGCTGCGGAGAGAGCTCTGCTGCTGAGAGGATGAGAGGATGAGAGGAC 780
 QY 952 TTTGAGCCCGGAGAGCTCAAAATCAAGACATCTCAGGGAAGAGCTCCACAGACATAT 1011
 Db 781 TTTGAGCCCGGAGAGCTCAAAATCAAGACATCTCAGGGAAGAGCTCCACAGACATAT 840
 QY 1012 GAAAGAGATCAACAGCAAAAGCTTCAAGGCGTGGGGCCAGCAAGTTCCATGGGTACGC 1071
 Db 841 GAAAGAGATCAACAGCAAAAGCTTCAAGGCGTGGGGCCAGCAAGTTCCATGGGTACGC 900
 QY 1072 TAGATGGAGATCTGGGATCATCGGCAAGACCTACAGAGAGGCGATGAGAGACATGAGCC 1131
 Db 901 TAGATGGAGATCTGGGATCATCGGCAAGACCTACAGAGAGGCGATGAGAGACATGAGCC 960
 QY 1132 AGTAGAGGACACAGCGGATTCAGAGACTTCAACATACAGAGACACAGCGTTGGCAATC 1191

Db 961 AGAGAGGACACGAGATCCAGACTTCACTACAGACACAGCGTGGCAAAATC 1020
 QY 1192 ATCTCATATGCTATAGAGAGACCACTTCTTGGGGTCAAGGTGTGTCGG 1251
 Db 1021 ATCTCATATGCTATAGAGAGACCACTTCTTGGGGTCAAGGTGTGTCGG 1080
 QY 1252 AACGGGAGAGATGGAGACCACTTAAATTTACTCAATTTCAAGACAGAGAGTGAAG 1311
 Db 1081 AACGGGAGAGATGGAGACCACTTAAATTTACTCAATTTCAAGACAGAGAGTGAAG 1140
 QY 1312 GTTCGGGATTAACAGCGGTGGTCTACACACTGGAGATCATCAATGACCACTAAAGTTTC 1371
 Db 1141 GTTCGGGATTAACAGCGGTGGTCTACACACTGGAGATCATCAATGACCACTAAAGTTTC 1200
 QY 1372 CAGGGGTCCGAGCCACCCAGAGACCACTTCTTGGAGAGTGGAGATCTCG 1431
 Db 1201 CAGGGGTCCGAGCCACCCAGAGACCACTTCTTGGAGAGTGGAGATCTCG 1260
 QY 1432 CTTCACATGATAGATCTGTCTGCTCTACACATCTCCGAGATGATGAGCCAGCGC 1491
 Db 1261 CTTCACATGATAGATCTGTCTGCTCTACACATCTCCGAGATGATGAGCCAGCGC 1320
 QY 1492 TTCTCTTCTTCAACATCAAGAGACCAAGACCAAGATTAAGATGATGAGCCCTAC 1551
 Db 1321 TTCTCTTCTTCAACATCAAGAGACCAAGACCAAGATTAAGATGATGAGCCCTAC 1380
 QY 1552 ATGAACAACTCATATCTCTGGGAGAGATGCTGTCTATGATCATCTCTCTTGGC 1611
 Db 1381 ATGAACAACTCATATCTCTGGGAGAGATGCTGTCTATGATCATCTCTCTTGGC 1440
 QY 1612 CTGATGAGGTCTCTGCTCAGAAAAAGACCTTTGAAACACTCTCAGCGTCCGAGACTGG 1671
 Db 1441 CTGATGAGGTCTCTGCTCAGAAAAAGACCTTTGAAACACTCTCAGCGTCCGAGACTGG 1500
 QY 1672 ATCTCATACGTGGGCTACACACACTGCTTTGGGGCATGTTTGAAGAGCTTGAAGGTC 1731
 Db 1501 ATCTCATACGTGGGCTACACACACTGCTTTGGGGCATGTTTGAAGAGCTTGAAGGTC 1560
 QY 1732 CATGCATCTTCAAAATGTAAGATGAAGAAAGATCATCAAGACAGAAAGCTGCTT 1791
 Db 1561 CATGCATCTTCAAAATGTAAGATGAAGAAAGATCATCAAGACAGAAAGCTGCTT 1620
 QY 1792 GTGATTTGGGGGGGCTGCTCTCATGACCTGTGATCTGATCTGTGGCAGGCTGTG 1851
 Db 1621 GTGATTTGGGGGGGCTGCTCTCATGACCTGTGATCTGATCTGTGGCAGGCTGTG 1680
 QY 1852 GACCCCTGGGAGAGACATAGAGAGTACAGCATGAGCGGACCCAGAGCCGGGAC 1911
 Db 1681 GACCCCTGGGAGAGACATAGAGAGTACAGCATGAGCGGACCCAGAGCCGGGAC 1740
 QY 1912 ATCTCATACGTGGGCTGTAAGACATGCGAAAAACCCACATGACCATGTGGCTTGGC 1971
 Db 1741 ATCTCATACGTGGGCTGTAAGACATGCGAAAAACCCACATGACCATGTGGCTTGGC 1800
 QY 1972 ATGCTACGCTACAGAGGGGCTCCCATGATCGGTTGTTCTTGGCATGGGAACC 2031
 Db 1801 ATGCTACGCTACAGAGGGGCTCCCATGATCGGTTGTTCTTGGCATGGGAACC 1860
 QY 2032 CGCAATGTAGCATCTCTGCTCTCAACGACAGCAAGTACATCGGATGAGTGTATAAT 2091
 Db 1861 CGCAATGTAGCATCTCTGCTCTCAACGACAGCAAGTACATCGGATGAGTGTATAAT 1920
 QY 2092 GTGGGATCATGATCATCTGAGGGGTGCTGCTCTCTCTGACGCGTGAACCCCAAC 2151
 Db 1921 GTGGGATCATGATCATCTGAGGGGTGCTGCTCTCTCTGACGCGTGAACCCCAAC 1980
 QY 2152 GTGCAATTTGCAATCGTGGCCCTGGTCAATCTTCTGACAGCATATCTCTGCTG 2211
 Db 1981 GTGCAATTTGCAATCGTGGCCCTGGTCAATCTTCTGACAGCATATCTCTGCTG 2040
 QY 2212 GTGTTTGTGCAAAAGCTCATATCTGAGAGACAAACCTGAGAGCCAGCTCAGAAAG 2271
 Db 2041 GTGTTTGTGCAAAAGCTCATATCTGAGAGACAAACCTGAGAGCCAGCTCAGAAAG 2100

QY 2272 CGGTTCCAGTTCACACAGACAGCAAGAAAGATTCGAAGACTTCAGTTCAGTCC 2331
 Db 2101 CGGTTCCAGTTCACACAGACAGCAAGAAAGATTCGAAGACTTCAGTTCAGTCC 2160
 QY 2332 AGCTTGAACAGGAG 2391
 Db 2161 AGCTTGAACAGGAG 2220
 QY 2392 CGAATGAGATCAGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2451
 Db 2221 CGAATGAGATCAGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
 QY 2452 ACACAG 2511
 Db 2281 ACACAG 2340
 QY 2512 AGCTTGGGAGAGTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2571
 Db 2341 AGCTTGGGAGAGTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
 QY 2572 GATCAAAACCCCGAGCTCCAGTGAAGACAGACAGAGAGAGAGAGAGAGAGAGAG 2631
 Db 2401 GATCAAAACCCCGAGCTCCAGTGAAGACAGACAGAGAGAGAGAGAGAGAGAGAG 2460
 QY 2632 ATGAAGAGATCAACTTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2691
 Db 2461 ATGAAGAGATCAACTTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
 QY 2692 CTTCACACAGCTTCACTCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 2751
 Db 2521 CTTCACACAGCTTCACTCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 2580
 QY 2752 GTGAGCCCTACGCGCCAGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
 Db 2581 GTGAGCCCTACGCGCCAGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
 QY 2812 TCGGGCCTGTAG 2823
 Db 2641 TCGGGCCTGTAG 2652

RESULT 7
 US-08-953-277-3
 ; Sequence 3, Application US/08953277
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Kenneth A.
 ; TITLE OF INVENTION: DNA ENCODING A GABAR2 POLYPEPTIDE AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 35
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/953,277
 ; FILING DATE: 17-OCT-1997
 ; CLASSIFICATION: 536
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 1795/54002/JPW/KDB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2652 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-953-277-3

Query Match 93.9%; Score 2650.4; DB 29; Length 2652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 172 ATGGGCTCATGCGCTGCTCCAGAGAGGTGGCCAGAGGAGCAATCCGGGCGCGCGCTGCTC 231
DB 1 ATGGGCTCATGCGCTGCTCCAGAGAGGTGGCCAGAGGAGCAATCCGGGCGCGCGCTGCTC 60
QY 232 CCGCGCTGAGAGTACCATCGAGCAGATCCGCAAGCAAGTCACTCTGCGCCCTACTTC 291
DB 61 CCGCGCTGAGAGTACCATCGAGCAGATCCGCAAGCAAGTCACTCTGCGCCCTACTTC 120
QY 292 CTGACCTGAGACTGATATGACACGAGTGTGACATGCAATGCAAGGAGCTGAAAGCTCTAT 351
DB 121 CTGACCTGAGACTGATATGACACGAGTGTGACATGCAATGCAAGGAGCTGAAAGCTCTAT 180
QY 352 GAGCAATAAAGTATGGGCGCAACATTGATGTGTTTGGAGGCGTGTGCTGCTGTC 411
DB 181 GAGCAATAAAGTATGGGCGCAACATTGATGTGTTTGGAGGCGTGTGCTGCTGTC 240
QY 412 ACATATATTATGCGGAGATCCCTCCAGAGCTGGAATCGGTGCGCTTCTCTCGCGCC 471
DB 241 ACATATATTATGCGGAGATCCCTCCAGAGCTGGAATCGGTGCGCTTCTCTCGCGCC 300
QY 472 ACCAGCCCTGCTTCTCGGATTAAGAAAGTACCCGTAATTTCTTCGGAGCGTGCCGTCA 531
DB 301 ACCAGCCCTGCTTCTCGGATTAAGAAAGTACCCGTAATTTCTTCGGAGCGTGCCGTCA 360
QY 532 GACAAGCGGTGAACCCCGCATCTCTGAAGCTCTGGAAGCACTCCGCTGGCGGCTGTG 591
DB 361 GACAAGCGGTGAACCCCGCATCTCTGAAGCTCTGGAAGCACTCCGCTGGCGGCTGTG 420
QY 592 GGCACACTCAGCAGAGCTGACGCGCTTCTCCAGGTGAGAAATGACCTGACTGGGGTT 651
DB 421 GGCACACTCAGCAGAGCTGACGCGCTTCTCCAGGTGAGAAATGACCTGACTGGGGTT 480
QY 652 CTGTATGGGAGATATTGATCTCAGACACAGAGATTCTCCAAATGATCCCTGCACC 711
DB 481 CTGTATGGGAGATATTGATCTCAGACACAGAGATTCTCCAAATGATCCCTGCACC 540
QY 712 AGGCTCAAAAAGTCAAGGGGAATGACGTGGGATCATCTTGCCAGTTTGACAGAAAT 771
DB 541 AGGCTCAAAAAGTCAAGGGGAATGACGTGGGATCATCTTGCCAGTTTGACAGAAAT 600
QY 772 ATGGCAGCAAAAAGTCTTCTGTGTGCTTCCAGAGAGACATGTTTGACAGAGTACAG 831
DB 601 ATGGCAGCAAAAAGTCTTCTGTGTGCTTCCAGAGAGACATGTTTGACAGAGTACAG 660
QY 832 TGGATATATCCCGGAGATGATGACAGGCTCGTGTGGAGAGAGTGTGGAGGGCAAT 891
DB 661 TGGATATATCCCGGAGATGATGACAGGCTCGTGTGGAGAGAGTGTGGAGGGCAAT 720
QY 892 TCCCTACGCTGCTGCGCAGAAAGCTCTGCTGCCATGAGAGATTAACATCGAGTGTGAC 951
DB 721 TCCCTACGCTGCTGCGCAGAAAGCTCTGCTGCCATGAGAGTTCATCGAGTGTGAC 780
QY 952 TTGAGAGCCCTGAGCTGCAAAACAATCAAGACATCTTCAGAGGAAGTCCACAGCGTAT 1011
DB 781 TTGAGAGCCCTGAGCTGCAAAACAATCAAGACATCTTCAGAGGAAGTCCACAGCGTAT 840
QY 1012 GAAAGAGATGACAAAGCAAGCGTTCAGGCGTGGGGCCAGCAAGTTCATGGGTACGCC 1071

DB 841 GAAAGAGATGACAAAGCAAGCGTTCAGGCGTGGGGCCAGCAAGTTCATGGGTACGCC 900
QY 1072 TACGATGGGATCTGGGTCAATGCGCAAGACCTTAAGAGAGGAGCCATGAGACTCATGCC 1131
DB 901 TACGATGGGATCTGGGTCAATGCGCAAGACCTTAAGAGAGGAGCCATGAGACTCATGCC 960
QY 1132 AGTACAGAGCACACGCGGATTCAGAGACTTCACTACACAGACACACCTTGGCAAAATC 1191
DB 961 AGTACAGAGCACACGCGGATTCAGAGACTTCACTACACAGACACACCTTGGCAAAATC 1020
QY 1192 ATCTCAATGCGCATGAACGAGACCAACTTCTCGGGGTACGCGGTCAAGTGTCTCCG 1251
DB 1021 ATCTCAATGCGCATGAACGAGACCAACTTCTCGGGGTACGCGGTCAAGTGTCTCCG 1080
QY 1252 AACGGGAGAGAAATGGGAGACATTAATTTACATTTCAAGACAGAGAGAGTGAAG 1311
DB 1081 AACGGGAGAGAAATGGGAGACATTAATTTACATTTCAAGACAGAGAGAGTGAAG 1140
QY 1312 GTGCGCAATCAACGCGGTGCTGACACACTGAGATCATCATGACACCATTAAGTTTC 1371
DB 1141 GTGCGCAATCAACGCGGTGCTGACACACTGAGATCATCATGACACCATTAAGTTTC 1200
QY 1372 CAGGGTCCGAGCCACCCAGACAGACCATCATCTGAGAGACCTTCCGAGAGATCTCG 1431
DB 1201 CAGGGTCCGAGCCACCCAGACAGACCATCATCTGAGAGACCTTCCGAGAGATCTCG 1260
QY 1432 CTTCACATGATATGACATCTGTCCGCTCACACATCTCGCATGATGATGAGCGGCC 1491
DB 1261 CTTCACATGATATGACATCTGTCCGCTCACACATCTCGCATGATGATGAGCGGCC 1320
QY 1492 TTCCTCTCTTCAACATCAAGAACCGGAGACCAAAAGCTGATTAAGATGTCAGAGCCCTAC 1551
DB 1321 TTCCTCTCTTCAACATCAAGAACCGGAGACCAAAAGCTGATTAAGATGTCAGAGCCCTAC 1380
QY 1552 ATGAACAACCTCATCATCTGAGAGAGATGCTGCTATGATCATCTTCTCTTTGGC 1611
DB 1381 ATGAACAACCTCATCATCTGAGAGAGATGCTGCTATGATCATCTTCTCTTTGGC 1440
QY 1612 CTGATGAGGTCTCTGCTGCTGAGAAAAGACCTTGAAGAACTGTGACAGGTCCGAGCTGG 1671
DB 1441 CTGATGAGGTCTCTGCTGCTGAGAAAAGACCTTGAAGAACTGTGACAGGTCCGAGCTGG 1500
QY 1672 ATTCTCACCGTGGCTACACAACTGCTTTGGGCGCATGTTTGCAAAACCTGAGAGGTC 1731
DB 1501 ATTCTCACCGTGGCTACACAACTGCTTTGGGCGCATGTTTGCAAAACCTGAGAGGTC 1560
QY 1732 CATGCCATCTTCAAAAATGTAAGATGAAGAAGAGATCATCAAAAGACCAAGACTGCTT 1791
DB 1561 CATGCCATCTTCAAAAATGTAAGATGAAGAAGAGATCATCAAAAGACCAAGACTGCTT 1620
QY 1792 GTGATTTGGGGGCGATGCTGCTCATGACCTGTGATCTCTATCTGTTGGCAGAGCTGTG 1851
DB 1621 GTGATTTGGGGGCGATGCTGCTCATGACCTGTGATCTCTATCTGTTGGCAGAGCTGTG 1680
QY 1852 GACCCCTGCGGAGACAGTGAAGAGTACAGCATGAGACCGGACCCGAGCGCGGAC 1911
DB 1681 GACCCCTGCGGAGACAGTGAAGAGTACAGCATGAGACCGGACCCGAGCGCGGAC 1740
QY 1912 ATCTCATCCGCCCATGCTGAGAACACTGGAAGAACACCCACATATACCATGCTGGC 1971
DB 1741 ATCTCATCCGCCCATGCTGAGAACACTGGAAGAACACCCACATATCATCTGCTGGC 1800
QY 1972 ATTGCTACGCGCTCAAGAGGAGCTCTCATATGCTATTCGTTTCTTGCCATGGGAAAC 2031
DB 1801 ATTGCTACGCGCTCAAGAGGAGCTCTCATATGCTATTCGTTTCTTGCCATGGGAAAC 1860
QY 2032 CGCAATGTAAGACATCCCGCCCTCAAGACAGCAAGATTAATGAGATGATGATTAAT 2091
DB 1861 CGCAATGTAAGACATCCCGCCCTCAAGACAGCAAGATTAATGAGATGATGATTAAT 1920
QY 2092 GTGGGATCATGTCATCATGCGGGGTGCTGCTCTTCTGACCGCTGACACCCCAAC 2151

Db	1921	GTGGGATCATATGTGCATCATCATCGGAGCGCTGCTGTCTCTCTCTCCCTCGAGCGGTGACACCGCCAAAC	1985
QY	2152	GTGCAAGTTCTGTGATCTGTGAGGGCCCTGGTGCATCATCTTCTGACAGACACATCACTCTCTGGCTG	2211
Db	1981	GTGCACATTTCTGATCTGTGAGGGCCCTGGTGCATCATCTTCTGACAGACACATCACTCTCTGGCTG	2040
QY	2212	GTGTTTGTGTCCAAAGCTCATTTACTCTTGAGGACAAACCTTGACGACGCCATCATGAAACAGG	2271
Db	2041	GTGTTTGTGTCCAAAGCTCATTTACTCTTGAGGACAAACCTTGACGACGCCATCATGAAACAGG	2100
QY	2272	CGGTTTCAGTTTCACACAGAAACCAAGAAAGAAATTTGAAAGACCTTCAGTTCAGTACAC	2331
Db	2101	CGGTTTCAGTTTCACACAGAAACCAAGAAAGAAATTTGAAAGACCTTCAGTTCAGTACAC	2180
QY	2332	AGCGTTGAAACGAGGCGAGCAGCTGACCGCTTGAGGAGACTGTGACATGACAAACACCGGCTT	2391
Db	2161	AGCGTTGAAACGAGGCGAGCAGCTGACCGCTTGAGGAGACTGTGACATGACAAACACCGGCTT	2220
QY	2392	CGAATGAAAGATTCACAGAGCTGTGACAAAGACTTGGAAAGAGTCACACATGACAGCTACAGAAC	2451
Db	2221	CGAATGAAAGATTCACAGAGCTGTGACAAAGACTTGGAAAGAGTCACACATGACAGCTACAGAAC	2280
QY	2452	ACACCGAGAGAGAGACCATATCATCAAAAGAAATCACTACCAAGAGCTCAACAGCAATCCGTC	2511
Db	2281	ACACCGAGAGAGAGACCATATCATCAAAAGAAATCACTACCAAGAGCTCAACAGCAATCCGTC	2340
QY	2512	AGCTTTGGGCACCTTTCACAGAGACAGATGAGAGAAAGGCCATTTCTAAAAAATCACCTC	2571
Db	2341	AGCTTTGGGCACCTTTCACAGAGAGACAGATGAGAGAAAGGCCATTTCTAAAAAATCACCTC	2400
QY	2572	GATCAAAACCCCCAGCTCAGTGAAGACAGACAGAGCCCTCAAAACATGCAAAAGACCC	2631
Db	2401	GATCAAAACCCCCAGCTCAGTGAAGACAGACAGAGCCCTCAAAACATGCAAAAGACCC	2480
QY	2632	ATGGAAGACATTAATTCCTCCGGAGACATTCAGAGCCGGGCTGTGGCTTCAGACTCCCATC	2691
Db	2461	ATGGAAGACATTAATTCCTCCGGAGACATTCAGAGCCGGGCTGTGGCTTCAGACTCCCATC	2520
QY	2692	CTTTCACACAGCCCTTACCTCCATCCATTCGAGAGCGGTGATGCGACAGCTCGTCAAGCCCTGT	2751
Db	2521	CTTTCACACAGCCCTTACCTCCATCCATTCGAGAGCGGTGATGCGACAGCTCGTCAAGCCCTGT	2580
QY	2752	GTTAGGCTTACAGGAGCCCTCGGACAGACAGACAGTACCAACCCCTCTTTCGAGTCATGGTC	2811
Db	2581	GTTAGGCTTACAGGAGCCCTCGGACAGACAGACAGTACCAACCCCTCTTTCGAGTCATGGTC	2640
QY	2812	TCGGGCGCTGTAG	2823
Db	2641	TCGGGCGCTGTAG	2652
<p> RESULT 8 PCT-US99-02361-1 : Sequence 1, Application PC/TUS9902361 : GENERAL INFORMATION: : APPLICANT: Merck & Co., Inc. : TITLE OF INVENTION: NOVEL GABAB RECEPTOR DNA SEQUENCES : FILE REFERENCE: 20052Y PCT : CURRENT APPLICATION NUMBER: PCT/US99/02361 : EARLIER FILING DATE: 1999-02-03 : EARLIER APPLICATION NUMBER: 60/073,767 : NUMBER OF SEQ ID NOS: 46 : SOFTWARE: FastSeq for Windows Version 3.0 : SEQ ID NO 1 : LENGTH: 3480 : TYPE: DNA : ORGANISM: Homo sapiens PCT-US99-02361-1 </p>			

Matches	2534;	Conservative	0;	Mismatches	288	Indels	3;	Gaps	1
QY	1	ATGGCTTCCCCCGGAGGTCGGGGGAGCCCGGGCGGGCGGCG--CCGGCGGCC	57						
Db	293	atggcttcccccgaggagctccggcagccggcgccggccggccacacggccgcc	352						
QY	58	GGCGGCTGCTGCTGCTCCCTGCTGTGCTGCTGCTGTGTGGCGCCGGGCTTGG	117						
Db	353	ggcgccctgctactactctctgctctgctgctgctgctgctctctggtccgggcttgg	412						
QY	118	GGCTGGAGCGGGGGGCGCCCGCGCGCGGCCGACAGCGCGCGCGCTCCATCATGGAG	177						
Db	413	ggctgggcgggggcgcccccgccggcgccgacggccggccgcttccatcaltgggc	472						
QY	178	CTCATGGCGGCTCACAGAGAGGTGGCCAGAGGGCAGCATGGGGCGGGCGTCCCGCCGCG	237						
Db	473	ctcatggcgcttccacaaaggatgggccaaggacagcaacggcgcggtgtgcccccgcc	532						
QY	238	GTGAGCTAGCCATCGAGAGAGATCCGACAGCAAGTACTCTTGGCGCCCTACTTCTGAC	297						
Db	533	gtgaaactggccactcagacagataccgcaagagttaactctgccccctacttcccagac	592						
QY	298	CTGGAGCTCTATACACCCGAGTGTGACATGCAAGAGGACGAAGGCTCTATATGACAG	357						
Db	593	ctggcgctctatgaacacggagtgcgacaacgaagggttgaaagctctctacggttga	652						
QY	358	ATTAAGTATGGCGCCCAACCATTTGATGTTTGGAGGCGCTGTCCGTGTGTACATCT	417						
Db	653	ataaataacggcgccgaacacacttgaagtggtlttgagggcgctgtccatccgacatccc	712						
QY	418	ATTATCGCGGAGTCCCTCCAGAGGCTGGATCTGTGTCAGCTTTCCTTCGGCGGACACAG	477						
Db	713	atcatctcagagcttccctcccaaggctggagatctggtgcagcttcttlttgcttcacacag	772						
QY	478	CCCTGCTCTCGGGATATGAAGAAAGATCCGATTTCTTCGCGAAGGGCCGTACAGCAAC	537						
Db	773	ccgtctctagcgaataaagaaaaataacctatattcttctggacgcgtcccatcagaacat	832						
QY	538	GGGGTGAACCCCGCATCTCTGAAGCTCTTGAAAGCATTCGCTGCGCGGCTGTGGGCA	597						
Db	833	ggggtgaaccccgcatcttgaagtgcttgcacaaagcactacgaatggaaagcggtggacag	892						
QY	598	CTCACGAGGAGCTGGACGCGCTTCTCCGAGGTGAGGAATGACACTGACTGGGGTTCGTAT	657						
Db	893	ctcagcgaaagcgttcaagaggtctctctgtgggtggtgcgaatgcacgtgactgtatctat	952						
QY	658	GGGGAAGATATTTGAGATCTCAGACACAGAGAGTATTTCCATATGATCCCTCCACAGGTC	717						
Db	953	ggggaaagatatttgagatcttcagacacggagagctcttcccaagatctccgttaccagtgct	1012						
QY	718	AAAAAGCTCAAGGGGAATGACGTGGGATCATCTTGTGCCAGTTTGAACCAAGATATGGCA	777						
Db	1013	aaaaagctcaagaggaaatgatagtctgcgaacatcttgcagcttlttgaccgaataatggca	1072						
QY	778	GCAAAAGCTCTTGTGTGTGCTCTCGAGGAGACATGTTTGGACACAGTATCCAGTGGATC	837						
Db	1073	gcaaaagtgtctctgtgtgtgatacagggggagcaactatgtgtatgtatlaatatcaagtgcac	1132						
QY	838	ATCCGGGATGTGTCAGAGCTGTGGTGTGGAGCAGGTGTCATGTGGAGGCCATTTCTCA	897						
Db	1133	atccgggctgtgtacgggctcttctgtgtgtggagcggtgacacaggaagccaactatccc	1192						
QY	898	GGTGTCTGGCGACAGAGCCCTCTGGCTGCCATGGAAGGTTCATCGGAGTGGACATTYTTGG	957						
Db	1193	gctgtgctccggaaagatctgtcttctgtccacatgaggggtctacatctgtgcgtgatttgcga	1252						
QY	958	CCCCGAGCTCTCAAAACAAATCAAGACCATCTATGGGAGAGACTCCACAGCGATATGAAGA	1017						
Db	1253	ccccgagcttccaaagcgatcaagagacatctcaagaaagacttccacagcgatagagaga	1312						
QY	1018	GAGTTCACAACAGCAACGTTTAAAGCGTGGGGCCGACAGTTCATGGGTATCGCTTACAT	1077						
Db	1313	gagttaacacaaagcgtgtcaaggctgtggggcccaagatttccaaaggttgaagcttaccat	1372						

QY	1078	GGATCTGGGTCATCCGCAAGACCTTCACGAGGGCCATGAGAACTCATGTCAGTATGC	1137
Db	1373	ggcatctgggtcatccgcaagacacatcgagagggccatgagaaactgatgcagcagc	1432
QY	1138	AGGCACACAGGGATCCAGACCTTCACATCACAGACACACAGCTGGGCAAAATCATCTCTC	1197
Db	1433	cggcacacaggcggaatccgagacttcaactacaagcacaagccagctgggcagagatcatctctc	1492
QY	1198	AATGCCATGAACGAGACCACTTCTTCGGGGTCACAGGGTCAAGTGTGTTCGGGAACGGG	1257
Db	1493	aatgccaatgaacgagaccactcttcctcggtgcacaggggtcaagtgtatctccgaaatggg	1552
QY	1258	GAGAGATAGGGAGACCATTAATTAATTACTCAATTTCAGSACACAAAGAGGGAAGGCGGC	1317
Db	1553	gagagataaggagaccatataattactcaattccaaagccagggaggtgaaagtggga	1612
QY	1318	GAATACACGCGGTGGCTGACACACTGGAGATCATCATACACCATTAAGTTCCAGGGG	1377
Db	1613	gaataaagaactgtyggccgacaactgagatcatcaatgacacacacgaagtccaaagga	1672
QY	1378	TCCGAGACCCACGACGACAGACCATCTTCGGAGCAGCGCTTCGGAGATCTCCGTCCTCA	1437
Db	1673	tccgaaacccaacaaagacagaccatcatctcgggcacaggggtcaagtgtatctccgaaatggg	1732
QY	1438	CTGTATAGATCTCTGTCGGCTCACCATCTCCGGCAGATGACATAGCGACAGCGCTTCCTC	1497
Db	1733	ctctaaagataccctctctgcctccccaatcccccgggaatgacatgagccaggtgtctctcc	1792
QY	1498	TTCTTTCACATCAAGAACCGGAAACAAAAGCTGATTAAGATGTCAAGCCCTCATGATGAC	1557
Db	1793	tcttcttaacatcaagaacccggaaatcagaagctcataaagaatgtagtcatcatcatagac	1852
QY	1558	AACTCATCATCTCCGGGAGSAAATGCTGTCTATGGATCATCATCTCCCTTGTGGCTGCAT	1617
Db	1853	aaactcatcatctcttgtagagatgctctccctcatgtcttcattctctcttgccctgat	1912
QY	1618	GGGTCTCTTGCTCAGAAAAGACTTGTGAACACTGTACAGCGTCGAGCCGAGCCGATGCTC	1677
Db	1913	ggatctcttgctctgtaagaagactcttgtaaaacttcgacacggtccagagactgattctcc	1972
QY	1678	ACCGTGGCTTACACACTGCCCTTGGGGCCATGTTGCAAAAGACTTGAAGGCTGCATGCTC	1737
Db	1973	accgtgggtctacaagcagcgtcttctgggccaatgtcttgcagaagacttgtagagatccacc	2032
QY	1738	ATTCTCAAAAATGTGAAGATGAGAGAAAGATCATCAAGAACCGAAGCTGCTTGATTT	1797
Db	2033	attctcaaaaatgtgaagaatgagaagaatcatcaagacagacagcagaaactgcttgatc	2092
QY	1798	GTGGGGGGCATGTCGCTCATCGACGCTGTGATCTGATCTGATCTGAGCGGTGTGAGACCC	1857
Db	2093	gtgggggggcatgctgctcatcgacgctgtgatctgatactggaatctgagcgtgctggagcccc	2152
QY	1858	CTGCGAGGACGATGAGAGAGTACACATGAGACCGGACCCAGACGCGGGACATCTCC	1917
Db	2153	ctgctgaaggaacgtgtggaagaatcacagatctgagcccgagccagaaggaacgggtatctcc	2212
QY	1918	ATCCGGCATTTGCTGGAACACTGCGAAAACACCCATGACATCACTGCTGGCATGTGC	1977
Db	2213	atccggcctcttccttggagcaactgtggaacaccatgaccatctgcttgcatctgc	2272
QY	1978	TACGCTTACAGGGGCTCTCATGCTATTCTCGTGTCTTCTGCGATGAGGAAACCGGCAAT	2037
Db	2273	tacgcttaaaaggactctctcaatgtcttcgggtgttctctagcttgggagaccggcaac	2332
QY	2038	GTGAGCATCCCTGCCTTCAACGACAGCAAGTACATCGGCATGACTGTGTCAATGTGGGG	2097
Db	2333	gtgagcatcccgccactcaacgacaagaatcatatcggatgagtggtctacaagctgggg	2392
QY	2098	ATCATGTGCATCATGGGGCTGCGTCTCTCTGACAGGCTGACACGCCCAAGCGTGCAG	2157
Db	2393	atacatgtgcatcatatcggggcgctgtctctctccctgacccgggacagccccaatgtgacg	2452

OY	2158	TTTGTGATGATGGCCCGTGGTATCATCTTCTTCACACATCAATCATCTCCATCCGCGATTT	22117
Db	2453	ttctgatcgtyggcttcgtytcatccttccttcgacacattcacctcttcgctgattcc	2512
OY	2218	GTTCCCAAACCTCATCTACTCTTGAGAGCAAAACCTGACAGACATCAAGAACAGGGGTTG	22777
Db	2513	gttccgaagctctatcaacccttgaacacaaaccagatcgaaagcaagcaggttc	25722
OY	2278	CAGTTGACACAGAACCAAGAAAGAAAGATTGGAAGACCTTCATCTTCACTACACACGTTG	23377
Db	2573	cagtttcaaccagatcaacgaagaagaagtcttaaaacgcttcacactggtctaccagtgty	26322
OY	2338	AACCAGGACGACGACGTCATCGGCTGGAGGGAGTCTGACAGTATAGAAAAACCGCCTTGAAATG	23977
Db	2633	aaccagacgagacatcccgctcgagggctctacagttcaagaaaccaatgctctggaaty	26922
OY	2398	AGATGACAGAGCTTGACAAAGACTTTGGAAAGTACATGCATGCAGTACAAAGACACCA	24577
Db	2693	aagatcacagagctgtgataaagacttgaagaggtcacatgcagctgcagagacacacca	27522
OY	2458	GAGAAAGCACATACATCAAAACAGAAATCACTACCAAGAGCTCAACGACATCTCAGCTTG	25177
Db	2753	gaaagacacacttatatlaaacgaagccactacacaaagatcgatgcatcttcaacctg	28122
OY	2518	GGCAACTTTACAGAGACGACACAGATGSGNAGAAAGCCATTCTTAAATAATCACTCATCA	25777
Db	2813	ggaacttcaactgaagagacagatggaaggaagcatttaaaaaaacctccgttcaa	28722
OY	2578	AAOCCCACTCTCACTGAGACACGACAGAGCCCTTCAGAACATGCAAAAGACCCCATAGAA	26377
Db	2873	aatccccaagtacagtygaaacaaacagagccctctgaaatgtcaaaagtccctataaga	29322
OY	2638	GACATCAATCTCCCGGACACATCAACGCGCGGTGTGCTCCAGCTCCGCATCTTCAC	26977
Db	2933	gataataactcttcagaacacatcacatcgatgctgtctccctcagctcccccattccac	29922
OY	2698	CAGCGCTACTCTCCATTCATCTGGAAGCGTGGATGCCAGCTTCGTCAAGCCCTGTGTCAAC	27577
Db	2993	cagcgctactctccatctcatcgagagcgtygagcgagctgttcagccccctgctcagc	30522
OY	2758	CCTAACCGCCAGCCCTCGGCGACAGACAGTACACACCCTCTCTTCAGAGCATAGTCTCGGGC	28177
Db	3053	cccacgcgaccccgccgacagaacatgctgcacccctcttcgagtcatgctctcgggc	31122
OY	2818	CTGTA 2822	
Db	3113	ctgta 3117	
RESULT	9		
	PCT-US99-11869-1		
	Sequence 1, Application PC/TUS9911869		
	GENERAL INFORMATION:		
	APPLICANT: United States of America, represented by Sec. HHS		
	APPLICANT: Clark, Janet		
	APPLICANT: Bonner, Tom I.		
	TITLE OF INVENTION: Memmalian g2b GABAB Receptors		
	FILE REFERENCE: 65879		
	CURRENT APPLICATION NUMBER: PCT/US99/11869		
	CURRENT FILING DATE: 1999-05-28		
	EARLIER APPLICATION NUMBER: 60/087, 274		
	EARLIER FILING DATE: 1998-05-29		
	NUMBER OF SEQ ID NOS: 30		
	SOFTWARE: FastSeq for Windows Version 3.0		
	SEQ ID NO 1		
	LENGTH: 5786		
	TYPE: DNA		
	ORGANISM: Homo sapiens		
	PCT-US99-11869-1		

Query Match	83.2%;	Score 2348.2;	DB 1;	Length 5786
Best Local Similarity	89.7%;	Pred. No. 0;		

[illegible]

QY 778 GCAAAAGTCTTGTGTGCTTTCGAGAGAGCATGTTTGGCAGCAAGTACCAGTGCATC 837
 Db 781 GCAAAAGTCTTGTGTGCTTTCGAGAGAGCATGTTTGGCAGCAAGTACCAGTGCATC 840
 QY 838 ATCCGGGATGTGAGAGCTGCTGGTGGAGCAGTGCATGATGAGAGCAATTCGCA 897
 Db 841 ATCCGGGATGTGAGAGCTGCTGGTGGAGCAGTGCATGATGAGAGCAATTCGCA 900
 QY 898 CGTGGCTGGCAGAGCTCTGCTGGTGGCAGTGAAGTTACATCGAGTGGACTTGGAG 957
 Db 901 CGTGGCTGGCAGAGCTCTGCTGGTGGCAGTGAAGTTACATCGAGTGGACTTGGAG 960
 QY 958 CCGCGAGCTCCCAACATTCAGACATCTCGAGGAGATCCACAGCAGATGAGAA 1017
 Db 961 CCGCGAGCTCCCAACATTCAGACATCTCGAGGAGATCCACAGCAGATGAGAA 1020
 QY 1018 GAGTACAAACAGCAAGCTTACGCGTGGGGCCAGCAAGTCCATGGTACGCTAGCAT 1077
 Db 1021 GAGTACAAACAGCAAGCTTACGCGTGGGGCCAGCAAGTCCATGGTACGCTAGCAT 1080
 QY 1078 GGGATCTGGGTATCGCCCAAGACCTTACAGAGGGCCATGAGACATCTGATGCCAGTACG 1137
 Db 1081 GGGATCTGGGTATCGCCCAAGACCTTACAGAGGGCCATGAGACATCTGATGCCAGTACG 1140
 QY 1138 AGGCAACAGCGGATCCAGAGCTTCACTACAGACACACGCTGGCCAAATCATCTCTC 1197
 Db 1141 CGGCAACAGCGGATCCAGAGCTTCACTACAGACACACGCTGGCCAAATCATCTCTC 1200
 QY 1198 AATGCCATGAGAGAGCAACTCTTTCGGGGTACGCGGTCAAGTTGTCTTCGGAAACGGG 1257
 Db 1201 AATGCCATGAGAGAGCAACTCTTTCGGGGTACGCGGTCAAGTTGTCTTCGGAAACGGG 1260
 QY 1258 GAGAAATGAGAGCAACTTAAATTTACTCAATTCAGAGAGAGAGTGAAGTGGCC 1317
 Db 1261 GAGAAATGAGAGCAACTTAAATTTACTCAATTCAGAGAGAGAGTGAAGTGGCC 1320
 QY 1318 GAATCAACAGCGGTGCTGACACACTGAGATCATCAATGACACCAATGATTCAGGGG 1377
 Db 1321 GAGTCAACAGCGGTGCTGACACACTGAGATCATCAATGACACCAATGATTCAGGGG 1380
 QY 1378 TCCGAGCCAGCAGAGAGCAAGCATATCTGAGAGAGCTTGGAGAGTTCGCGTTCCA 1437
 Db 1381 TCCGAGCCAGCAGAGAGCAAGCATATCTGAGAGAGCTTGGAGAGTTCGCGTTCCA 1440
 QY 1438 CTGTATACATCTCTGCTCGCTCTCCATCCATCTCGGATGATCAGCGCCCTTCTC 1497
 Db 1441 CTGTATACATCTCTGCTCGCTCTCCATCCATCTCGGATGATCAGCGCCCTTCTC 1500
 QY 1498 TTCTTCAACATCAAGAACCGGAGCAAGCTGATTAAGTGTCAAGCCCTACATGAGAC 1557
 Db 1501 TTCTTCAACATCAAGAACCGGAGCAAGCTGATTAAGTGTCAAGCCCTACATGAGAC 1560
 QY 1558 AACCTCATCATCTCTGAGAGAGATCTCTTATGATCATCTCTCTCTTGGCTGAT 1617
 Db 1561 AACCTCATCATCTCTGAGAGAGATCTCTTATGATCATCTCTCTCTTGGCTGAT 1620
 QY 1618 GGGTCTCTGCTGAGAAAGACCTTGAACACTGACAGGCTCGGACCTGAGATTCG 1677
 Db 1621 GGGTCTCTGCTGAGAAAGACCTTGAACACTGACAGGCTCGGACCTGAGATTCG 1680
 QY 1678 ACCGTGGGCTACCAACTGCTTTGGGGCCATGTTTGCAAAAGCTGAGAGGTCATGCGC 1737
 Db 1681 ACCGTGGGCTACCAACTGCTTTGGGGCCATGTTTGCAAAAGCTGAGAGGTCATGCGC 1740
 QY 1738 ATCTTCAAAATGTAAGATGAGAGAGATCATCAAAAGCCAGAGCTGCTGTGAT 1797
 Db 1741 ATCTTCAAAATGTAAGATGAGAGAGATCATCAAAAGCCAGAGCTGCTGTGAT 1800
 QY 1798 GTGGGGGAGATGCTCTATGAGACCTGATGATCTGATCTGTTGGAAGCTGTGAGCCG 1857
 Db 1801 GTGGGGGAGATGCTCTATGAGACCTGATGATCTGATCTGTTGGAAGCTGTGAGCCG 1860

QY 1858 CTGCGAGAGACAGTACAGAGTACAGATGAGCGCCGAGCCAGACAGCCGCGACATCTCC 1917
 Db 1861 CTGCGAGAGACAGTACAGAGTACAGATGAGCGCCGAGCCAGACAGCCGCGATCTCC 1920
 QY 1918 ATCCGCCATTTGCTGAGAACACTGCGAAACACCCACATGACCATCTGCTGGATGTC 1977
 Db 1921 ATCCGCCATTTGCTGAGAACACTGCGAAACACCCACATGACCATCTGCTGGATGTC 1980
 QY 1978 TACGCTTCAAGAGGCTCTCATGCTATTGCTGTTTCTTGGCATGAGAAACCCGCAAT 2037
 Db 1981 TACGCTTCAAGAGGCTCTCATGCTATTGCTGTTTCTTGGCATGAGAAACCCGCAAT 2040
 QY 2038 GTGAGCATCCCTGCTCAACAGCAGACAGATGATGAGCATGAGTGTGATGAGG 2097
 Db 2041 GTGAGCATCCCTGCTCAACAGCAGACAGATGATGAGCATGAGTGTGATGAGG 2100
 QY 2098 ATCATGTGATCATCGGGGCTGCTGCTCTCTTCCATGAGCGCTGACAGCCAGCTGAG 2157
 Db 2101 ATCATGTGATCATCGGGGCTGCTGCTCTCTTCCATGAGCGCTGACAGCCAGCTGAG 2160
 QY 2158 TTCTGATCTGAGGCTGCTGATCATCTTCTGACAGACCATCATCTCTGCTGCTGTT 2217
 Db 2161 TTCTGATCTGAGGCTGCTGATCATCTTCTGACAGACCATCATCTCTGCTGCTGTT 2220
 QY 2218 GTGCAAAAGCTCATCTCTGAGCAAAACCTGAGCGAGCGCATCGAAGACAGCGGTT 2277
 Db 2221 GTGCAAAAGCTCATCTCTGAGCAAAACCTGAGCGAGCGCATCGAAGACAGCGGTT 2280
 QY 2278 CAGTTCAACAGCAAGCAAGAAAGATTTGAAAGCTCCACTTCACTAGTACCAAGCTG 2337
 Db 2281 CAGTTCACTGCAATCAAGCAAGAAAGATTTGAAAGCTCCACTTCACTAGTACCAAGCTG 2340
 QY 2338 AACCAAGGAGAGCAAGTACAGCTTGGAGGAGTGCATGAGAAACACAGCCCTGCAATG 2397
 Db 2341 AACCAAGGAGAGCAAGTACAGCTTGGAGGAGTGCATGAGAAACACAGCCCTGCAATG 2400
 QY 2398 AAGATCAAGAGCTGACAGAAAGCTTGAAGAGTACCATGACAGTCAAGACACCA 2457
 Db 2401 AAGATCAAGAGCTGACAGAAAGCTTGAAGAGTACCATGACAGTCAAGACACCA 2460
 QY 2458 GAGAAAGACCATCATCAAGCAAGATCACTACCAAGAGCTCAACAGCATCTCAGCTTG 2517
 Db 2461 GAGAAAGACCATCATCAAGCAAGATCACTACCAAGAGCTCAACAGCATCTCAGCTTG 2520
 QY 2518 GGCACCTTACAGAGGACACAGATGAGAGAAAGCCATTTAAAAATTCACCTGATCAA 2577
 Db 2521 GGCACCTTACAGAGGACACAGATGAGAGAAAGCCATTTAAAAATTCACCTGATCAA 2580
 QY 2578 AACCCAGCTCCAGTGAAGACAGAGAGCCCTCAAGAACATGCAAGAGCCCATAGAA 2637
 Db 2581 AACCCAGCTCCAGTGAAGACAGAGAGCCCTCAAGAACATGCAAGAGCCCATAGAA 2640
 QY 2638 GACATCAACTCCCGGAGACATTCAGAGCCGCTGCTGCTCAGCTCCCATCTTCCAC 2697
 Db 2641 GACATCAACTCCCGGAGACATTCAGAGCCGCTGCTGCTCAGCTCCCATCTTCCAC 2700
 QY 2698 CAGCGCTACTCCCATCATCGAGAGGCTGATGATGACAGCTGCTGAGCCCTGATGAGC 2757
 Db 2701 CAGCGCTACTCCCATCATCGAGAGGCTGATGATGACAGCTGCTGAGCCCTGATGAGC 2760
 QY 2758 CCTACCGCAGACCCCTGCGCAGACAGACATCAACACCTCTCTCGAGTATGCTCGGGC 2817
 Db 2761 CCTACCGCAGACCCCTGCGCAGACAGACATCAACACCTCTCTCGAGTATGCTCGGGC 2820
 QY 2818 CTGTA 2822
 Db 2821 CTGTA 2825

RESULT 11
 US-09-211-755-46
 ; Sequence 46, Application US/09211755
 ; GENERAL INFORMATION:

Db 1501 TTCTCAACATCAAGAACCGGATCAGAGCTATAAGATGTGAGTTCATATCATGAAAC 1560
Oy 1558 AACCTCATCATCTGGAGAGATGCTGCTCATCATCATCTCTCTCTCTCTCTCTCTCT 1617
Db 1561 AACCTTATCATCTGGAGAGATGCTTCCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
Oy 1618 GGGTCTTGTCTCAGAAAAGACCTTGAACACTCTGCACGCTCCGAGCTGATCTC 1677
Db 1621 GGAATCTTGTCTCAGAAAAGACCTTGAACACTCTGCACGCTCCGAGCTGATCTC 1680
Oy 1678 ACCGTGGCTACAGAACTCTCTGGGAGCTATTTTGAAGAACTGAGAGCTCCATCC 1737
Db 1681 ACCGTGGCTACAGAACTCTCTGGGAGCTATTTTGAAGAACTGAGAGCTCCATCC 1740
Oy 1738 ATCTTCAAAATGTAAATGAAAGAAATCATCAAGAACTGAGAGCTCTGTGAT 1797
Db 1741 ATCTTCAAAATGTAAATGAAAGAAATCATCAAGAACTGAGAGCTCTGTGAT 1800
Oy 1798 GTGGGGGGGATGCTGCTCATGACCTGTGATCTGTGATCTGTGAGAGCTGAGACCC 1857
Db 1801 GTGGGGGGGATGCTGCTCATGACCTGTGATCTGTGATCTGTGAGAGCTGAGACCC 1860
Oy 1858 CTGGGAG 1917
Db 1861 CTGGGAG 1920
Oy 1918 ATCCGCCCATCTGTGAGAACTGCGAAACCCACATGACCTCTGTGATCTGTC 1977
Db 1921 ATCCGCCCATCTGTGAGAACTGCGAAACCCACATGACCTCTGTGATCTGTC 1980
Oy 1978 TAGCCCTACAG 2037
Db 1981 TAGCCCTACAG 2040
Oy 2038 GTGGAG 2097
Db 2041 GTGGAG 2100
Oy 2098 ATCATGTGATCATGCGGGGCTGCTGCTCTCTCTGAGCGGTGAGAGAGAGAGAG 2157
Db 2101 ATCATGTGATCATGCGGGGCTGCTGCTCTCTCTGAGCGGTGAGAGAGAGAGAG 2160
Oy 2158 TTCTGATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
Db 2161 TTCTGATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Oy 2218 GTGGCAAGCTCATTTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2277
Db 2221 GTGGCAAGCTCATTTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Oy 2278 CAGTTCACAG 2337
Db 2281 CAGTTCACAG 2340
Oy 2338 AACGAGGAG 2397
Db 2341 AACGAGGAG 2400
Oy 2398 AAGATCAG 2457
Db 2401 AAGATCAG 2460
Oy 2458 GAG 2517
Db 2461 GAG 2520
Oy 2518 GGCACCTTCACAG 2577
Db 2521 GGCACCTTCACAG 2580
Oy 2578 AACCCCGAGCTCAG 2637
Db 2581 AACCCCGAGCTCAG 2640

Oy 2638 GACATCAATCCCGGAG 2697
Db 2641 GATATAATCTCCAG 2700
Oy 2698 CAGGCTTACCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 2757
Db 2701 CAGGCTTACCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 2760
Oy 2758 CCAACCGAG 2817
Db 2761 CCAACCGAG 2820
Oy 2818 CTGTA 2822
Db 2821 CTGTA 2825

RESULT 12
US-09-390-134-30
Sequence 30, Application US/09390134
GENERAL INFORMATION:
APPLICANT: BARNES, ASHLEY A.
APPLICANT: WISE, ALAN
APPLICANT: MARSHALL, FIONA H.
APPLICANT: FRASER, NEIL J.
APPLICANT: WHITE, JULIE H. M.
APPLICANT: FORD, STEVEN M.
TITLE OF INVENTION: NOVEL RECEPTOR
FILE REFERENCE: P63558052
CURRENT APPLICATION NUMBER: US/09/390.134
CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: GB9819420.2
EARLIER FILING DATE: 1998-09-07
EARLIER APPLICATION NUMBER: 60/103.570
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 2826
TYPE: DNA
ORGANISM: Homo sapiens
US-09-390-134-30

Query Match 83.1%, Score 2346.6, DB 52; Length 2826;
Best Local Similarity 89.7%, Pred. No. 0;
Matches 2533; Conservative 0; Mismatches 289; Indels 3; Gaps 1;
Oy 1 ATGGCTTCCCGGAG 57
Db 1 atggcttcccgaggag 60
Oy 58 GCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 117
Db 61 gcgcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 120
Oy 118 GCGTACGCGGAG 177
Db 121 gcgtagcgag 180
Oy 178 CTATGCGGCTACAG 237
Db 181 ctatgctgctacag 240
Oy 238 GTGAGAGTACAG 297
Db 241 gtgagagctacag 300
Oy 298 CTGGAGCTTATGACAG 357
Db 301 ctggagcttataag 360

Db	2521	ggaactctcagtagagacagatctggaagaagcgccattttaaaaaatcaactctgcac	2580
QY	2578	AACCCCACTCCACTGAGACAGACAGAGCCCTCAAGACATGCAGACGCCCATAGAA	2637
Db	2581	aatccccagctacagctggaatacaaaagagccctctcgaaatacgaagaatccctaaagaa	2640
QY	2638	GAGCATCACTCCCCGAGACATCCAGCGCGGCTGTGCTCCAGTCCCATCTTCAC	2697
Db	2641	gataataactcttcagaaacacatccagctcgtccctccagctcccatctccac	2700
QY	2698	CAGGCTACTCCCTCCATCCATCGAGAGCGGTGAGATGCCACTGCTGCAAGCCCTGTGCAGC	2757
Db	2701	caagcctacccctccatccatccgcgagctgtagaacgctgtgtctcaagccctcgcgcagac	2760
QY	2758	CCCTACCGCCAGGCCCTCGGCACAGACAGTACCAACCTCTCTTCGAGTCAATGATCTCGGGC	2817
Db	2761	ccccacgcagacgccccgcacaaagacatctgtcacacctctctcgagtcacatgtctcgcgc	2820
QY	2818	CTGTGA 2822	
Db	2821	ctgtga 2825	

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RESULT 13
US-60-172-373-2106
: Sequence 2106, Application US/60172373
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
: FILE REFERENCE: GX-0006 P
: CURRENT APPLICATION NUMBER: US/60/172,373
: CURRENT FILING DATE: 1999-12-16
: NUMBER OF SEQ ID NOS: 25,772
: SOFTWARE: PERL Program
: SEQ ID NO 2106
: LENGTH: 5787
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc:feature
: OTHER INFORMATION: Incyte ID No: 231654.4
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 276-304, 784, 3575-3607, 4217-4234, 4612
: OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-2106

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Query Match	82.58;	Score 2329.4;	DB 87;	Length 5787;
Best Local Similarity	89.78;	Pred. No. 0;		
Matches 2536; Conservative	0;	Mismatches 286;	Indels 5;	Gaps 3

[illegible]

Dh	698	gtggaactcgtgcatacgcagcagatccgcgaacgacgtaactctctgcgccctactcttcgtac	757
Qy	298	cttccgacactcttctmgaacaccgagttgtg- caatggcaaaagsgactaaagcctttatnagaagc	356
Dh	758	cgtgcgcctctatgacacgaggtgtgcancacgcaaaaggttgaagccttctacatgac	817
Qy	357	aatnagaatnagggccgaaccatttgatggtgttttggagggctgttcctgttcacatc	416
Dh	818	aaataaatatcggcgccgaacacttgaatgtgttttggaggtctctgtccatccgttaacatc	877
Qy	417	tattatnagggagatccctccaaaggcgaatnagtgatcttccctgtgcgccacacac	476
Dh	878	calcatatgaggtctccccaagcgtcgatcttgttgagcttcttcttgcgaacac	937
Qy	477	gcctgtttcttgagatnagaagaatcccgatatttctccgaagcgtccgttcagaca	536
Dh	938	gctcgtctcaagcagatataagaaaaaataccctatcttcttcgacgcgtccatcagaaca	997
Qy	537	cgcgctgaacccccgacactctcgaagctcctgnaagcattccgcgtgcggcgtgtggac	596
Dh	998	tgcgtgtaatccagcaltctgagttgtctcaagcactcaagtgaaagcgtgtggac	1057
Qy	597	actnagcagcagcgcagcagcgttctccagatnagagatnagctgcacgtgggtttcta	656
Dh	1058	gtcgaagcagaagcgttccaggtgtctcttgaggtgagaaagacgtacgtcgtgttcgtta	1117
Qy	657	tggggaagatattagatcttcaacacacagagtttctccatnagatccctgcacacagct	716
Dh	1118	tgcgagagacatttgatatttccagacacgagagcttctccaaagatccctctgacatglt	1177
Qy	717	caaaaagctcagaggagatgactnaggagatcactcttggccagtttgaccagaaatnagtc	776
Dh	1178	caaaaagctgaaggagatgattgtgcgatactcttcgtccagtttgaccagaaatnagtc	1237
Qy	777	agcaaaagcttcttggctgttcagagagagcattgtttggcagaagatnagcagatnag	836
Dh	1238	agcaaaagcttcttgcgtgtgtgcatacagagagagacatgtatgtgtgataataatccgtgat	1297
Qy	837	catnccggagatgtatcgaagcctgcgtgtgtggagcagcagctcatnaggagccaatncttc	896
Dh	1298	catnccggagctgtgtacgagccttctctgtgtggagagaggtgtcacacgaaacacacatc	1357
Qy	897	acgtctcctgtgcacaaagccctcctgcgtcccatnagaaagttatctgaaatggacttttga	956
Dh	1358	ccgtgcctccggaagatctgtctgtgcatacgtgagggctatactgtgcgtgatttcga	1417
Qy	957	gccccgactctccaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac	1016
Dh	1418	gccccgagcttccaagcagaacaaagacatcttccaagaaagcctccaagacagatcgaag	1477
Qy	1017	agagtaacaaacagacggttcaagcgttgagggccacgaagttccatnaggatccctacga	1076
Dh	1478	agagtaacaaacagcaggttcaagcgttgcagggccagaaagttccaagcgttccatcaga	1537
Qy	1077	tggagatctggagatcctgcgaacacccccaacagagggccatnagagacatgagatcccgatg	1136
Dh	1538	tgcgacatctgtgtcgtccaaagacacgtcgaaggggcattgagagacatgtatgcgaagc	1597
Qy	1137	caggacacagcggatcgaagacttcaactncaacacacacacacacacacacacacacac	1196
Dh	1598	ccgagccacggagatcccgagcttcaactacacaggaacacacacacacacacacacac	1657
Qy	1197	caatgccatgaacgagacacacttcttgcgggctcaggggtcaagtttgcgttcggaacg	1256
Dh	1658	caatgccatgaacgagacacacttcttgcgggctcaggggtcaagtttgcgttcggaatg	1717
Qy	1257	ggagagaaatggcaacacatttaatttactcaatttcaacacacacacacacacacacac	1316
Dh	1718	ggagagaaatgggagacatttaatttactcaatttcaacacacacacacacacacacac	1777
Qy	1317	cgaaatnagcggcgtgtgcacacatcgaagatcatcaatnagcactaaagtttccaggg	1376
Dh	1778	agagtaacacgctgtgtgcgcgaacacacacacacacacacacacacacacacacac	1837

```

OY 1377 GTCGAGCCACCAGCAAGACCATATTCAGAGACCTTCGGAAATCTCGCTCC 1436
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Db 1838 atccgacacacacacacacacacacacacacacacacacacacacacacac 1897
OY 1437 ACCTGATACACATCTCTCCGCTCTACCATCTCTGCGATATATATGCGCTTCT 1436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1898 tccctacacacacacacacacacacacacacacacacacacacacacacac 1957
OY 1497 CTTCCTTCAACATCAAGAACCGGAACCAAAAGCTGATTAGATGCAAGCCCTACATGAA 1556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1958 ctctctcaacacacacacacacacacacacacacacacacacacacacacac 2017
OY 1557 CAACCTCATCATCTGGGAGGAGAGCTGCTGCTATGATCCATCTCTCTTGGCTGGA 1616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2018 caacctcatcatctctctctctctctctctctctctctctctctctctct 2077
OY 1617 TGGGCTCTCTGCTCAGAAAAGACCTTTGAAAACCTCTGACGGTCCGAGCTGATTTCT 1676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2078 tggatcctctctctctctctctctctctctctctctctctctctctctct 2137
OY 1677 CACCGTGGGCTACACAACTGCTTGGGGCCATGTTTGAAGACCTGGAGGTCATGAC 1736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2138 caccgtgggctacacacacacacacacacacacacacacacacacacacac 2197
OY 1737 CATCTTCAAAAATGTGAAGATGAGAGAGAAATCATCAAGACCAACACTGCTGTGAT 1796
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2198 catcttcaaaaatgtgaagatgagagagaaatcatcaagacacaaactgtgtgat 2257
OY 1797 TGTGGGGGGCATGCTGCTCATCGACCTGTGATCTGATCTGTTGGACAGCTGTGAGACC 1856
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2258 cgtggggggcatgctgctcatcgacctgtgatctgttggacagctgtgagacc 2317
OY 1857 CCGTGGGAGGACAGTAAAGAGTAAAGAGTAAAGAGTAAAGAGTAAAGAGTAAAGAGTAAAG 1916
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2318 cctgggaaagagacagtgagagagagagagagagagagagagagagagagag 2377
OY 1917 CATCGCCCATTTGCTGGAACACTCGGAAAACCCACATGACATCTGCTTGGCATTTGT 1976
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2378 catcgcccatcttctctctctctctctctctctctctctctctctctctct 2437
OY 1977 CTACGCTTCAAGAGGGGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2036
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2438 ctatgctctcaagagagagagagagagagagagagagagagagagagagag 2497
OY 2037 TGTGAGCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2096
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2498 cgtgagcatccctgagacacacacacacacacacacacacacacacacac 2557
OY 2097 GATCATGTGATCATCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2558 gatcatgtgatcatctctctctctctctctctctctctctctctctctctct 2617
OY 2157 GTTCCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2618 gtctctgacatctctctctctctctctctctctctctctctctctctctct 2677
OY 2217 TGTGCAAAAGCTGATT-ACCTGAGAGCAAACTGAGCAGCAGCTCAAGAACGGCGGT 2275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2678 cgtgcaaaagctgattacacacacacacacacacacacacacacacacacac 2737
OY 2276 TCCAGTTCAACAGAAACAGAAAGAAATGGAAGAGCTCTCACTTATGATGACAGAG 2335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2738 tccagttcaacagaaacagaaagaaagaaagaaagaaagaaagaaagaaag 2797
OY 2336 TGAACCAAGCGAGACAGCTACGCTGAGAGAGCTGAGTCAAGAAAACACCGCTTTCGAA 2395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2798 tgaaccaagcgagacacacacacacacacacacacacacacacacacacac 2857
OY 2396 TGAAGATCAAGAGCTGAGCAAAAGCTTGAAGAGTCAACATGACGCTACAAAGACACAC 2455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2858 tgaagatcaagagctgagtaagaccttgagagaggtcacacatgacgtcgagagacac 2917

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OY 2456 CAGAGAGACACATACATCAAAACAGAAATCACTACCAAGAGCTCAAGACATCTGAGCT 2515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2918 cagaaaagacacacacacacacacacacacacacacacacacacacacacac 2977
OY 2516 TGGGCACTTCAAGAGACACAGATGAGAAAGGCAATCTTCAAAATCAACCTGATAC 2575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2978 tgggcaacttcaagagacacagatgagaaagaaagaaagaaagaaagaaagaa 3037
OY 2576 AAAACCCCAAGCTCCAGTGAACACAGAGAGCCCTCAAGAACATGCAAGAACCCATGAC 2635
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3038 aaaatcccaagctcagtgagaaacacacacagacccctcgaagatgcaagatgcatag 3097
OY 2636 AAGATCAACATCTCCGAGAGACATCTCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2695
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3098 aagatataaactctcagagacacacacacacacacacacacacacacacacac 3157
OY 2696 AGCAGGCTTACCTCCATCTCATCTGAGAGGCTGATGCCAGCTGCTGAGCCCTGTGTCA 2755
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3158 accagcctacacacacacacacacacacacacacacacacacacacacacac 3217
OY 2756 GCCCTACCGCAGCCCTCGCAGACAGACAGTACCAACCTCTTCCAGATGATGCTCGG 2815
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3218 gccccacgcgcagcccccgcacagacatgycacacccctctccagatgcatgtctcg 3277
OY 2816 GCCCTGA 2822
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3278 gccctga 3284

RESULT 14
PCT-US99-11869-28
; Sequence 28, Application PC/TUS9911869
; GENERAL INFORMATION:
; APPLICANT: United States of America, represented by Sec. HHS
; APPLICANT: Bonner, Tom I.
; APPLICANT: Clark, Janet.
; TITLE OF INVENTION: Mammalian gp2 GABAB Receptors
; FILE REFERENCE: 658/9
; CURRENT APPLICATION NUMBER: PCT/US99/11869
; EARLIEST FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087, 274
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ. ID NOS: 30
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ. ID NO 28
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-11869-28

Query Match      81.9%; Score 2311; DB 1; Length 3396;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 2498; Conservative 0; Mismatches 290; Indels 3; Gaps 1;
OY 1 ATGGCTTCCCGCGAGCTCCGGGACACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 atggcttcccgagctccgggacacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 517
OY 58 GCGGCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 gcgcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 577
OY 118 GCGTGGAGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 578 ggcgtggcgcgggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 637
OY 178 CTATGCCGCTTCAAGAGAGTGGCAAGGCGAGCATGGGCGCGGCTGCTCCCGCGC 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 638 ctatgccgcttcaagagagtggtgcaagggcgagcgagcgagcgagcgagcgagcgagcg 697
OY 238 GTGAGCTACGCTACGAGCATCGCAACGAGTACTGCTGCGCCCTACTCTCTGAGAC 297
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```

Dd 698 gtggaactgcatcgagcagatcgcgaagtcactccgcgccctactccctgac 757
Qy 298 CTGGACTATGACACCGAGTGTGACAAATGCAAGGAGACTGAAGCCCTTCTATGACGA 357
Dd 758 ctgcgctctatgacacgagctgcgaacgcaaaaggcttgaaagccttataagatgca 817
Qy 358 ATAAAGATGAGGCGGAACCATTTGATGATGTGAGAGGCTGTGCGCTGTGCATATCT 417
Dd 818 ataaataacgagccgaacacattgagtgttggagagcgctcttccatccgttactcc 877
Qy 418 ATATCGCGAGTCCCTCCAAAGGCTGGAATCTGTGACGCTTTCCTTCCGCCCAACG 477
Dd 878 atcatctgacagctccccaagctggaatctgtgcagcttcttctgtgcacaacg 937
Qy 478 CCTGCTTTCGCGATGAAGAGATACCCGATTTCTTCCGAGGCTGCTGACGACAC 537
Dd 938 cctgtcttagcagataaagaaaaataccttattcttcttggaacgctccatcagaacat 997
Qy 538 GCGGTGAACCCCGCATCTCTGAAGCTCTGAAAGCACTTCCGTGGCGGCTGTGGGACA 597
Dd 998 gcggtgataccagccattctgaagtgtctcaagcactacacagtggaagcgctgggacg 1057
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Dd 1058 ctgcagcaagaagcttcagaggtctctgaggtgcgaatgacctgactgagctgtctat 1117
Qy 658 GGGGAAATATTTGAGATCTCAGACAGAGAGTTTCTCAATGATCCTCGACAGCGCTC 717
Dd 1118 ggcagagacatlgagatltcagacacgagagcttcccaagatccctgtacacagctc 1177
Qy 718 AAAAGCTCAAGGGGAATGACGTGCGGATCATCTTGGCAGTTTGACAGAAATNTGCA 777
Dd 1178 aaaaagctgaagggaaatgctgcgcatcactctgscagtttgacagaataatgca 1237
Qy 778 GCAAAATCTTCTGTTGCTGCTTCCCTGAGAGAGATGTTGGCAGAAATACATACAGATC 837
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Qy 1078 GGGATCTGGGTCTATCGCCAAAGACCTTACAGAGGCGCATGAGACCTCATGCGCAATGAC 1137
Dd 1538 ggcattctgtgtcatcgcgaagacatgcagaggtgcattgagacatctgacgtcagaagc 1597
Qy 1138 AGGCAACGCGGATCCAGACTTCAACTACACAGACCAACGCTGCGCAAAATCATCTC 1197
Dd 1598 cggacccagcgatccagagcttcaactacagcagaccacacgcttgagagatcatctc 1657
Qy 1198 AATGCCATGAACGAGCAACTTCTCGGGGTACAGGGTCAAGTGTGTCCGGAAGCGG 1257
Dd 1658 aatgcagaaagcagacaaactcttcgggtcagcgggtcaagttgttctccggatggg 1717
Qy 1258 GAGAGAAATGGGAACCATTAATTTACTCAATTTCAAGACAGCAGAGAGTGAAGTCCGC 1317
Dd 1718 gagagaatgggagacatlaaattactcaattcacaagacagcagggatgtaaggtggga 1777
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Dd 1778 gagtacaacgctgtgcgacacactgagatcatcaatgacacatcaaggttccaagga 1837

Qy 1378 TCCGAGCCACCCAGAGCAACACATCTATTCTGAGACAGCTTGGGAAGATCTCGCTTCCA 1437
Dd 1838 tccgaaccacacaaagacaaagacacatcctccttgagaaagctgcgaaagatcctccactc 1897
Qy 1438 CTGATAGCATCTCTGCTCCCTCTCACCATCTCTCGGAGATGATCATGAGCGAGCTCTC 1497
Dd 1898 ctctacagatcctctctcctccatccatcctcggatgatacatgacagctgtcttctcc 1957
Qy 1498 TTCTTCAACATCAAGAACCGGAAACCAAAAGCTGATTAAGATGTCTAGCCCTTCAATGAA 1557
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Qy 1618 GGGTCTCTCTCAAGAAAGACCTTGAACACTCTGACAGGCTCCGAGCTGGATTTCTC 1677
Dd 2078 ggaaccttctctcgaaaaagaccttgaacacacttgaacacgctcgaagaccgtgactc 2137
Qy 1678 ACCGTGGGCTACCAACATCCTTTGGGGCATGTTTGCAAAAGACCTGAGGCTCATGTC 1737
Dd 2138 accgtgggtacacgacgcttcttgaggcatgtttgaaagacctgagagatccacgccc 2197
Qy 1738 ATCTTCAAAATGTGAAGATGAAGAAAGATCATCAAAAGCCGAAGCTTGTGATTT 1797
Dd 2198 attctcaaaaatgtaaaatgaaagaagatcatcaagacccaagaaactgctgtgact 2257
Qy 1798 GTGGGGGCTGCTGCTCATCGACTGTGCATCTGATCTGTGAGAGCTGTGACCCC 1857
Dd 2258 gtgggggcatctgtctgtatcgaacctgtgtatcgtactgtcgtgcagctgtggacctc 2317
Qy 1858 CTGGGAGGACATAGAGAGTACAGCATAGAGCGCGGACCCAGACGCGGAGCATCTCC 1917
Dd 2318 ctgcgaagagcaatgtagaagaatgatacagatcagatgcagccagagagacggatattcc 2377
Qy 1918 ATCCGCCATTTGCTGGAACACTGCGCAAAACCCACATGACCATCTGTGGCTTGGCTTGTCTC 1977
Dd 2378 attccgctctctcttgagacatctgtagaacacccatagacatctgtctgtgcatctgtc 2437
Qy 1978 TACGCTTCAAGGGGCTCTCATGCTATTCGTTGTTCTTGGCATGGAAACCGCAT 2037
Dd 2438 tatgctcaaaaggaacttctcaatgtgtctgtgtcttcttctgtgtgtggagaccggac 2497
Qy 2038 GTAGCATCTCCCTGCTCAACGACAGCAAGTACATCGCATGATGTGTACATGTGGG 2097
Dd 2498 gtacagatctcccgcaactcaacagacagcaagatcatcgtgaltgtctcaacagctggg 2557
Qy 2098 ATCATGTGATCATTCGGGCTGTGTCTCTCTCTGACGCGTGCACAGCCAAAGTGCAG 2157
Dd 2558 atcatgtcatctatctgggctgcgtgtcttctctctcctgcagcggacagcccaatgtgcag 2617
Qy 2158 TTCTGATCTGTGGCTGCTGATCATCTTCTGTGACACCATCATCTCTCTGCTGTGT 2217
Dd 2618 ttctgtcatctgtgtctgtgtcatcattctgtcagcacacatccctctcctgtgtatc 2677
Qy 2218 GTGCAAGGCTCATTTACTGTGAGAACAACTCTGACGAGCACTGTCAAGAACGCGGTT 2277
Dd 2678 gtgcggaagctcatccactcctgtgaacaaacccagatgacgaacgcaagacagcgatctc 2737
Qy 2278 CAGTTACAGAGAACGAGAAAGAAAGATTGAGAGCACTTCACTTCAAGTACACAGGCT 2337
Dd 2738 cagttctcatgaatcagaagaagaagatcttcaaaacgttccatccatctgtccatcagctg 2797
Qy 2338 AACCAAGCGAGACGTACGCTGAGGAGTGTGATGAGAAACCAACCGCTTGAATG 2397
Dd 2798 aaccaagccagacatcccgctgtggagctctacagtcagaanaacatcgcctgtgcatg 2857
Qy 2398 AAGATTCAGAGGTGGGCAAGACTGTGAAGAGTCACTATGACGCTATCAAGACACACCA 2457
Dd 2858 aagatcacaagctgtgataaagacttggaaaggttcaacatgacgctgcgagacacaca 2517

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THE

WORLD

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 11:46:08 ; Search time 1755.56 Seconds

(without alignments)
6071.396 Million cell updates/sec

Title: US-09-211-755-3

Sequence: 2823
1 ATGGCTCCCGCCGAGATC.....TCATGCTCCGCGGCGCTGTAG 2823

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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2: em_est2:*
3: em_est3:*
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103: gb_est84:*
104: gb_est85:*
105: gb_est86:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	345	12.2	397	43	A1214087 ap29g06.x
2	304.2	10.8	704	63	A1968032 wu12c11.x
3	293.2	10.4	371	22	H14151 ym62d04.f1
4	257.4	9.1	341	20	Z43654 HSC1H041.n
5	230.6	8.2	560	45	A1341249 qx90d04.x
6	203.6	7.2	368	20	T07621 EST05511.pe
7	202.8	7.2	853	87	A0744524 HS_5508_A

BASE COUNT	87 a	102 c	83 g	66 t	3 others
ORIGIN					
Query Match	9.1%; Score 257.4; DB 20; Length 341;				
Best Local Similarity	88.3%; Pred. No. 3.2e-39;				
Matches 301; Conservative	0; Mismatches 38; Indels 2; Gaps 2;				
QY 2074	GGCATGAGTGTGACAAATGTGGGATCATATGACATACATACGAGGCGTGTGCTTCCTCCG 2133				
DB 1	GGATGAGTGTCTACACACTGGGGATCATATGATCATATCAGGCGCTGTCTCTCTTCG 60				
OY 2134	ACGGGTGACACGACCCACAGTTCGATTCGATCGGCGCTTGTCATCATCTTTCGACG 2193				
DB 61	ACCGGGGACACGAGCCCATGTGATTCGATTCGATTCGCTGTGTCATCATCTTTCGACG 120				
OY 2194	ACCATCATCTCTGCGCTGTGTTTGTGCAAGTTCATTCCTGTGAGACCAACCTGAC 2253				
DB 121	ACCATCATCCCTTCGCTGTGTTTGTGCAAGTTCATTCCTGTGAGACCAACCTGAGAT 180				
OY 2254	GCAGCCACTGAG-AACAGGCGGTTCCATTTACACAGAACCAAGAAAGAGATTTCGA 2312				
DB 181	GCACCAACGAGAAACAGGCGATTCCATTTACCAATCAGAAAGAAAGAAAGATTTCGA 240				
OY 2313	GACCTCCACTTCAGTCCACGAGCGGTGACACGAGGAGCAGCTCAAGCGCT-GGAGGACATCC 2371				
DB 241	AACGTCACCTCCGTTGTCACGATGTGAAACCAAGCCAGACACATCCCGCTGGAGGCGCTAC 300				
OY 2372	AGTCAGAAACACGCGCTTCGATGAGATGACAGAGCG 2412				
DB 301	AGTCAGAAACCATCCCTTCGCAATGAAATCAGATCAGAGCGT 341				
RESULT 5					
AI341249/c					
LOCUS	AI341249 560 bp mRNA EST 15-FEB-1999				
DEFINITION	G990004.x1 NC1_CGAP-GC6 Homo sapiens cDNA clone IMAGE:2009767 3', mRNA sequence.				
ACCESSION	AI341249				
VERSION	AI341249.1 GI:4078176				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
AUTHORS	Butleris; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 560)				
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT	National Cancer Institute, Cancer genome Anatomy Project (CGAP), Tumor Gene Index				
	Unpublished (1997)				
	On Jan 14, 1998 this sequence version replaced gi:1798073.				
	Contact: Robert Strausberg, Ph.D.				
	Email: Robert.L.Strausberg@nih.gov				
	Tissue Procurement: Christopher A. Moskajuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.				
	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.				
	cDNA Library Arrayed by: Greg Lennon, Ph.D.				
	DNA Sequencing by: Washington University Genome Sequencing Center				
	Clone distribution: NCI-CGAP clone distribution information can be				
	found through the I.M.A.G.E. Consortium/DBLNL at:				
	www.bio.lnhi.gov/dbtrp/image/image.html				
	Insert Length: 1613 Std Error: 0.00				
	Seq. primer: -400P from Gldco				
	High quality sequence stop: 452.				
FEATURES	Location/Qualifiers				

wp78g11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467940 3'

RNA sequence.

ACCESSION AI937563
VERSION AI937563.1 GI:5676433

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE

1 (bases 1 to 416)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/RTGAP), Tumor Gene Index
Unpublished (1998)

JOURNAL

COMMENT
On Jun 5, 1998 this sequence version replaced gi:3187952.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
www.bio.linn.gov/dbp/image/image.html

FEATURES

Seq primer: -400P from Gibco.
Location/Qualifiers

source

1..416
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2467940"
/clone_lib="NCI CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGAGGCGGCGGAGGATGTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."BASE COUNT 72 a 127 c 130 g 86 t 1 others
ORIGIN

Query Match

Best Local Similarity 93.7%; Score 113.8; DB 63; Length 416;
Pred. No. 4,6e-12; Mismatches 8; Indels 0; Gaps 0;

Matches 118; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY

2697 CCACGGCTACCTCCATCCATCGAGGCGTGGATGCGAGTGGTGTGAG 2756
|||||

DB

416 CCACGGCTACCTCCATCCATCGAGGCGTGGATGCGAGTGGTGTGAG 357
|||||

QY

2757 CCTACCGGCGAGCGCTCGGCGACAGACAGTACCACTCTTCGAGTATGTCGGG 2816
|||||

DB

356 CCCACCGGCGAGCGCTCGGCGACAGACATGTGCCACTCTTCGAGTATGTCGGG 297
|||||

QY

2817 CCTGTA 2822
|||||

DB

296 CCTGTA 291
|||||

RESULT 12

AI500214 414 bp mRNA EST 14-APR-1999
LOCUS AI500214/c
DEFINITION tm94a05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2105744 3',
mrna sequence.
ACCESSION AI500214

VERSION AI500214.1 GI:4392196

EST.

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE

1 (bases 1 to 414)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/RTGAP), Tumor Gene Index
Unpublished (1998)

JOURNAL

COMMENT
On Mar 20, 1998 this sequence version replaced gi:2980163.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
www.bio.linn.gov/dbp/image/image.htmlInsert Length: 506 Std Error: 0.00
Seq primer: -400P from Gibco.

FEATURES

Location/Qualifiers

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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGAGGCGGCGGAGGATGTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."BASE COUNT 74 a 127 c 128 g 84 t 1 others
ORIGIN

Query Match

Best Local Similarity 91.9%; Score 108.6; DB 47; Length 414;
Pred. No. 4,4e-11; Mismatches 10; Indels 0; Gaps 0;

Matches 114; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY

2699 ACAGCTACCTCCATCCATCGAGGCGTGGATGCGAGTGGTGTGAG 2758
|||||

DB

414 ACAGCTACCTCCATCCATCGAGGCGTGGATGCGAGTGGTGTGAG 355
|||||

QY

2759 CTACCGGCGAGCGCTCGGCGACAGACAGTACCACTCTTCGAGTATGTCGGG 2818
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DB

354 CCACCGGCGAGCGCTCGGCGACAGACATGTGCCACTCTTCGAGTATGTCGGG 295
|||||

QY

2819 TGTGTA 2822
|||||

DB

294 TGTGTA 291
|||||

RESULT 13

AM049355 512 bp mRNA EST 18-SEP-1999
LOCUS AM049355/c
DEFINITION UI-M-BH1-ane-a-02-0-UT s1 NIH BMAP M.S2 Mus musculus cDNA clone
UI-M-BH1-ane-a-02-0-UT 3', mRNA sequence.
ACCESSION AM049355
VERSION AM049355.1 GI:5909884

KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 512)
Bonaldo, M.F., Lennon, G., and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Mar 16, 1998 this sequence version replaced gi:2961822.
Contact: Chn, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLY-A-NO.

FEATURES

source location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-ane-a-02-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pUT3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 3,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB="NIH_BMAP_M_S2"
TAG_TISSUE="Prefrontal-cortex"
TAG_SEQ="GCTCA"

BASE COUNT 121 a 132 c 133 g 126 t
ORIGIN

Query Match 3.6%; Score 102.2; DB 64; Length 512;
Best Local Similarity 57.8%; Pred. No. 7.5e-10;
Matches 182; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

Db 331 CATTACCGCTCTGTCACCATGATCCCTTCCAGCCAGACGACCCCTTCCTTC 272
Qy 2169 GGGCTGGATCATCATCTGTGACGACCATCATCTGCTGGCTGTGTCACCAAGCT 2228
Db 271 CTCTGCGCATTTGTTCTTCTCTCATATTACTCTGTTGCTCTTTCGCTAAGAT 212
Qy 2229 CATTTACTGTGAGAC 2243
Db 211 GCGCAGGTGATCAC 197

RESULT 14
AM158263
LOCUS 393 bp mRNA EST 05-NOV-1998
DEFINITION za39b08.x1 Xenopus EST library Xenopus laevis cDNA clone za39b08
5', mRNA sequence.
ACCESSION AM158263
VERSION AM158263.1 GI:6270292
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae;
Xenopus.

REFERENCE 1 (bases 1 to 393)
Schutz, R., de la Bastide, M., Huang, E.N., Nascimento, L., Preston, R.,
Shah, R., Swaby, L., Shekher, M., Spiegel, L., Vall, M.D. and
McCombie, W.R.
Expressed sequence tags from Xenopus
Unpublished (1999)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cs.hlb.org
Plate: za39 row: b column: 08
Seq primer: M13 universal forward primer
High quality sequence stop: 393.
Location/Qualifiers
1..393

FEATURES

source location/Qualifiers
1..393
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="za39b08"
/clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
/tissue="W22-TGA"
/cell_line="tadpole"
/dev_stage="tadpole"
/note="Vector: lambda zap I; Site_1: XbaI; This library
was supplied by Holly Cline (Cold Spring Harbor Labs).
cDNA synthesis with oligo dt Xba I (Xba I cloning site).
RNA: stage 50-56 tadpoles, total brain tissue, GTC
extraction method."

BASE COUNT 94 a 98 c 91 g 110 t
ORIGIN

Query Match 3.4%; Score 95.4; DB 71; Length 393;
Best Local Similarity 54.8%; Pred. No. 1.3e-08;
Matches 189; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Db 151 AGCTGGAACCTGACATCTTCTCAAGATGACACATGCTGCTATATGCTCTA 210
 QY 1988 AGGGGCTCTCATGCTATTCGGTGTCTTCTGGCATGGAAACCCGCATGTGAGCATCC 2047
 Db 211 AAGGGCTACTCTTCTGCTGCTATATCTTCTGCTATGACACCAAGAGTTCACACG 270
 QY 2048 CTGGCTCAAGACAGCAGATGATCGGATGAGTGTACATGATGAGGATCATGCA 2107
 Db 271 AGAAGATCATGACACCGCTGCTGGGATGCGATATATACATGTGCTGCTTGGC 330
 QY 2108 TCATCGGGGCTGCTGCTCTTCTGACGCGTGACCAAGCCACG 2152
 Db 331 TCATCACCGCTCGACGACATGATCTCAGTACGACACGACG 375

RESULT 15

AA567648

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA567648 404 bp mRNA EST 28-NOV-1998
 H101578: 5prime HL Drosophila melanogaster head Bluescript
 Drosophila melanogaster cDNA clone H101578 5prime, mRNA sequence.
 AA567648
 AA567648.1 GI:2340430
 EST.
 fruit fly.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 404)
 Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
 Brokstein, P., Lewis, S. and Rubin, G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (1997)
 On Sep 12, 1996 this sequence version replaced gi:1394839.
 Contact: Harvey, D.
 G. M. Rubin-Molecular and Cell Biology
 University of California Berkeley
 539 USA, Berkeley, CA 94720-3200, USA
 Fax: 510 643 9947
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: 15 row: G column: 6
 High quality sequence stop: 379.
 Location/Qualifiers
 1. 404
 /organism="Drosophila melanogaster"
 /db_xref="BDGP_EST:BDc1n022505"
 /db_xref="taxon:7227"
 /clone="H101578"
 /clone_1id="HL Drosophila melanogaster head Bluescript"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="SOLR"
 /note="Organ: head-Brain & sensory organ; Vector:
 Bluescript SK; Site_1: EcoRI; Site_2: XhoI; Constructed
 using Stratagene ZAP-cDNA Synthesis kit. Oligo dt-primed
 and directionally cloned at EcoRI and XhoI in Bluescript
 SK(+/-)"

BASE COUNT

105 a 90 c 88 g 121 t

ORIGIN

Query Match 3.3%; Score 94.2; DB 35; Length 404;
 Best Local Similarity 54.9%; Pred. No. 2.3e-08;
 Matches 186; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 1374 GGGGTCGAGCCAGCAGACATCTTCTGAGCAGCTTCGAGATCTCGCT 1433
 Db 66 GGGGAAACCTCTCCAGAGATCGACCTTGATCTACATCGACAGTCAGTCAATCC 125
 QY 1434 TCACATGTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1493
 Db 126 AACCATATATGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185

QY 1494 CCTCTTCTTCAACATCAAGAACCGGAACCAAGCTGATTAAGATGTCAGCCCTACAT 1553
 Db 186 TCTGCGCTTAACTAATTAAGATGCAATCAAGATCAAGATGTCAGCTCCATTT 245
 QY 1554 GAACACCTCATCTCTGAGAGAAATGCTGCTGATGATCATCTCTCTTGGCT 1613
 Db 246 GAACATCTGATCATGAGGCTGTATGATGATGATGATGATGATGATGATGATGAT 305
 QY 1614 CGATGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1673
 Db 306 GCAATCAATTAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
 QY 1674 TCTCACGCTGAGCTACACAACTGCTTGGGGCCATGTT 1712
 Db 366 CTGATGCTGCTGATTCAGTCTCAGTTTGGAGCCATGTT 404

Search completed: March 16, 2000, 11:46:20
 Job time: 1887 sec

(W.I.)

```

Mpsrch_pp    protein - protein database search, using Smith-Waterman algorithm
Run on:      Wed Mar 15 22:13:59 2000;      MasPar time 99.69 Seconds
Tabular output not generated.              653.783 Million cell updates/sec

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Title:	>US-09-211-755-4
Description:	(1-940) from US09211755.pep
Perfect Score:	6906
Sequence:	1 MASPPSSQPPPPPPPPA.....TASRRHHVPPSTRVMSGL 940

Scoring table: PAM 150

Searched: 225878 seqs, 69334122 residues

Listing first 45 summaries

Database:

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 54.925; Variance 104.973; scale 0.523

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	6894	99.8	940	11	068871	GABA-B RECEPTOR G32.	0.00e+00
2	6772	98.1	941	4	075899	GABA-B RECEPTOR.	0.00e+00
3	2234	32.3	1211	5	09Y133	BCDNA.GH07312.	0.00e+00
4	1684	24.4	844	4	096022	GABAB RECEPTOR, SUBUNIT	0.00e+00
5	1680	24.4	812	11	096308	GABAB RECEPTOR, ID.	0.00e+00
6	1681	24.3	833	11	09WV15	573K1.1.2 (GAMMA-MINIO	0.00e+00
7	1681	24.3	844	11	09WV17	573K1.1.2 (GAMMA-MINIO	0.00e+00
8	1680	24.3	844	11	086521	GABA-BRIE RECEPTOR.	0.00e+00
9	1676	24.3	899	4	095975	GABAB RECEPTOR, SUBUNIT	0.00e+00
10	1675	24.3	961	4	095375	GABA-B1A RECEPTOR.	0.00e+00
11	1671	24.3	930	4	095468	GABA-B1A RECEPTOR.	0.00e+00
12	1673	24.2	960	11	09WV18	573K1.1.1 (GAMMA-MINIO	0.00e+00
13	1672	24.2	960	11	096620	GABA-B1A RECEPTOR.	0.00e+00
14	1671	24.2	960	11	09WU48	GABA-B1A RECEPTOR.	0.00e+00
15	1371	24.2	211	11	075975	GABA-B1A RECEPTOR.	0.00e+00
16	1350	19.5	662	11	09WV16	GABA-B1A RECEPTOR.	0.00e+00
17	1341	19.5	875	11	09Z0F9	GABA-B1A RECEPTOR.	0.00e+00
18	1349	19.4	991	11	09Z0U4	GABAB RECEPTOR SUBTYPE	3.10e-25
19	1163	16.8	182	4	075974	GABAB RECEPTOR SPLIC	1.68e-11
20	720	10.4	402	5	Q23444	COSMID Z1180.	1.34e-11

45	158	2.3	84.4	13	0.93552	POTATIVE COOANT REEP
44	160	2.3	84.0	11	0.9208	POTATIVE TASTE RECEPT
43	161	2.3	84.0	11	0.9208	POTATIVE TASTE RECEPT
42	165	2.4	84.0	11	0.9208	POTATIVE TASTE RECEPT
41	167	2.4	84.0	11	0.9208	POTATIVE TASTE RECEPT
40	164	2.4	84.0	11	0.9208	POTATIVE TASTE RECEPT
39	173	2.5	85.6	13	0.93553	POTATIVE COOANT REEP
38	170	2.5	85.6	13	0.93553	POTATIVE COOANT REEP
37	180	2.6	86.4	13	0.93553	POTATIVE COOANT REEP
36	180	2.6	86.4	13	0.93553	POTATIVE COOANT REEP
35	181	2.6	86.4	13	0.93553	POTATIVE COOANT REEP
34	179	2.6	86.4	13	0.93553	POTATIVE COOANT REEP
33	184	2.7	87.1	13	0.93554	POTATIVE COOANT REEP
32	190	2.8	88.9	10	0.92078	POTATIVE COOANT REEP
31	194	2.8	89.8	10	0.92078	POTATIVE COOANT REEP
30	190	2.8	89.8	10	0.92078	POTATIVE COOANT REEP
29	202	2.9	90.6	10	0.92078	POTATIVE COOANT REEP
28	202	2.9	90.6	10	0.92078	POTATIVE COOANT REEP
27	212	3.1	94.0	10	0.92078	POTATIVE COOANT REEP
26	216	3.1	94.0	10	0.92078	POTATIVE COOANT REEP
25	217	3.1	94.0	10	0.92078	POTATIVE COOANT REEP
24	231	3.3	90.8	4	0.95945	POTATIVE ION CHANNEL P
23	231	3.3	90.8	4	0.95945	POTATIVE ION CHANNEL P
22	252	3.6	95.3	10	0.92675	POTATIVE ION CHANNEL P
21	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
20	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
19	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
18	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
17	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
16	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
15	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
14	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
13	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
12	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
11	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
10	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
9	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
8	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
7	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
6	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
5	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
4	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
3	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
2	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P
1	259	3.7	95.8	10	0.92675	POTATIVE ION CHANNEL P

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	940 AA.
ID	088871;			
AC	088871;			
DT	01-NOV-1998 (TRENDEL)	08,		
DT	01-NOV-1998 (TRENDEL)	08,		
DT	01-MAY-1999 (TRENDEL)	10,		
DE	GABA-B RECEPTOR GB2			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=CEREBRAL CORTEX;			
RA	CLARK J.C., LAM A., BONNER T.I.;			
RT	"gb2, A second GABA-B receptor".			
RL	Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: A058575; AAC33954.1;			
DR	PFAM: PF01003; Tm3.1.			
DR	PFAM: PF01094; ANF_Receptor; 1.			
SO	SEQUENCE 940 AA; 105762 MW; 94C83CC1 CRC32;			

Query Match	99.88;	Score 6894;	DB 11;	Length 940;
-------------	--------	-------------	--------	-------------

Matches 938; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db	1	MAPPSSGQPPPPPPPPARLLPLPLSTLLMLTAGMGWTRGAPPPSSPPLSINGL	60
Oy	1	MAPPSSGQPPPPPPPPARLLPLPLSTLLMLTAGMGWTRGAPPPSSPPLSINGL	60
Db	61	MLPTEVAKSGISGVLPAVELAIQIRNSLLRPFLDRLPYTEDCNAGKGLKAFYAI	120
Oy	61	MLPTEVAKSGISGVLPAVELAIQIRNSLLRPFLDRLPYTEDCNAGKGLKAFYAI	120
Db	121	KGFPHMLWREGVGCVSVSTSLAESLOGNVLQVLSFAATPYLAARKKPYPFPPYPSNA	180
Oy	121	KGFPHMLWREGVGCVSVSTSLAESLOGNVLQVLSFAATPYLAARKKPYPFPPYPSNA	180
Db	181	VNPAILKLKLEFFRRRVGVLLYDDXOFSEVRYNDLVGYLGDIEISDTSEFSNDPCTSYK	240
Oy	181	VNPAILKLKLEFFRRRVGVLLYDDXOFSEVRYNDLVGYLGDIEISDTSEFSNDPCTSYK	240
Db	241	KLKGDVRIILGQFDONMAKXVFCCEAESMEFSKQWILPGWEPAMQVYVEANSR	300
Oy	241	KLKGDVRIILGQFDONMAKXVFCCEAESMEFSKQWILPGWEPAMQVYVEANSR	300

Db 301 CTRSLAAMEGYIGVDEPLSSKOIKTISGKTPOOEFEREYNSKRGVGPSPKFGHAYDG 360
 Qy 301 CTRSLAAMEGYIGVDEPLSSKOIKTISGKTPOOEFEREYNSKRGVGPSPKFGHAYDG 360
 Db 361 IWTIAKTLOPAMETLHASSRHORIODENVYDHTLGLKILNANNEFVGYGVVERNGE 420
 Qy 361 IWTIAKTLOPAMETLHASSRHORIODENVYDHTLGLKILNANNEFVGYGVVERNGE 420
 Db 421 RMGTFKTFODSREYKVEYNAVADTLEIINDTIRFQSGSEPPKDTIILEQKRISLPL 480
 Qy 421 RMGTFKTFODSREYKVEYNAVADTLEIINDTIRFQSGSEPPKDTIILEQKRISLPL 480
 Db 481 YSILSALTILGIMASAFLEFNIRKRNOKLIKMSPPYNNLLILGMLSYASIFLFGIDG 540
 Qy 481 YSILSALTILGIMASAFLEFNIRKRNOKLIKMSPPYNNLLILGMLSYASIFLFGIDG 540
 Db 541 SEVSEKTEFTLCTVRWTLVGYTAFSGAMFAKTWRVHAIFKNVKKKKIKDKLLVY 600
 Qy 541 SEVSEKTEFTLCTVRWTLVGYTAFSGAMFAKTWRVHAIFKNVKKKKIKDKLLVY 600
 Db 601 GGMILIDCILLICQWAVDELRTVERYSMEPPDPAGRDISIRPLEGENTHMTIMGLIV 660
 Qy 601 GGMILIDCILLICQWAVDELRTVERYSMEPPDPAGRDISIRPLEGENTHMTIMGLIV 660
 Db 661 AYKGLMLFEGCFIAMETRVNSIPALNSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 720
 Qy 661 AYKGLMLFEGCFIAMETRVNSIPALNSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 720
 Db 721 CIYALVLIIFCSTLTLCLVEFVPLILTKTNPDAONRFOFTONOKKEDSKTSTVSYN 780
 Qy 721 CIYALVLIIFCSTLTLCLVEFVPLILTKTNPDAONRFOFTONOKKEDSKTSTVSYN 780
 Db 781 QASTSRLEGQSNHRLRKITELDKDLEETMLODOPPEKTYIKONHGOELNDLSIG 840
 Qy 781 QASTSRLEGQSNHRLRKITELDKDLEETMLODOPPEKTYIKONHGOELNDLSIG 840
 Db 841 NFTSTSTGGAAILKNHLDONPOLONTTEPRTCKDPLEDINSEHIOQLSLQPLIHH 900
 Qy 841 NFTSTSTGGAAILKNHLDONPOLONTTEPRTCKDPLEDINSEHIOQLSLQPLIHH 900
 Db 901 AYLPISIGVDASCPVSPASPRHRHVPPSFVRVWSGL 940
 Qy 901 AYLPISIGVDASCPVSPASPRHRHVPPSFVRVWSGL 940
 RESULT 2
 ID 075899 PRELIMINARY: PRT: 941 AA.
 AC 075899:
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)
 DE GABA-B RECEPTOR.
 GN GABAB-R2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA CLARK J.C., LAM A., BONNER T.I.;
 RT "902, a second GABA-B receptor";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CEREBELLUM;
 RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,
 RA BARNES A.A., EASON P., FOORD S.M., MARSHALL F.H.;
 RT "heterodimerisation is required to form a functional GABAB receptor";
 RL Submitted (OCT-1998) to EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HIPOCAMPUS;

RA BOROWSKY B., LAZ T., GERALD C.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HIPOCAMPUS;
 RA BOROWSKY B., LAZ T., GERALD C.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF056085; AAC63228.1; -
 DR EMBL; AJ012188; CA09942.1; -
 DR EMBL; AF074483; AAD03336.1; -
 DR PFM; PF00003; 7tm.3; 1.
 DR PFM; PF01094; ANF_receptor; 1.
 KW Signal; Receptor
 SQ SEQUENCE 941 AA: 105821 MW: 83861 DLF CRC32;
 Query Match 98.1%; Score 6772; DB 4; Length 941;
 Best Local Similarity 97.8%; Pred. No. 0.00e+00;
 Matches 920; Conservative 15; Mismatches 5; Indels 1; Gaps 1;
 Db 1 MASRSSGQGPPEPPPPARLLILLPLPLPLAGAMGAMGAPRPPSSPPISMG 60
 Qy 1 MASPPSSGQGPPEPPPPARLLILLPLPLPLAGAMGAMGAPRPPSSPPISMG 59
 Db 61 LMPITKEVAGSGTGRVLAVALAEIQRNLSLRPFYDLRLYDTRCONAKLAFYA 120
 Qy 61 LMPITKEVAGSGTGRVLAVALAEIQRNLSLRPFYDLRLYDTRCONAKLAFYA 119
 Db 121 IKYPNHLMVFGVCPSPVSTIAESLQGMNVLVSFAATPVLDKRRKYPYFRTVPSDN 180
 Qy 120 IKYPNHLMVFGVCPSPVSTIAESLQGMNVLVSFAATPVLDKRRKYPYFRTVPSDN 179
 Db 181 AVNPAIKLKLKHOMKRVGLTQDOVRFSEVRNDLTGLYGEDIEIDTSPSFNDPCTSV 240
 Qy 180 AVNPAIKLKLKHOMKRVGLTQDOVRFSEVRNDLTGLYGEDIEIDTSPSFNDPCTSV 239
 Db 241 KKLGNVVRILLQFQONNAAYFCCAYEEMNGSKTOMIIPGHPYSWMEQYHTANSS 300
 Qy 240 KKLGNVVRILLQFQONNAAYFCCAYEEMNGSKTOMIIPGHPYSWMEQYHTANSS 299
 Db 301 FCLRNLLAAMEGYIGVDEPLSSKOIKTISGKTPOOEFEREYNSKRGVGPSPKFGHAYD 360
 Qy 300 FCLRNLLAAMEGYIGVDEPLSSKOIKTISGKTPOOEFEREYNSKRGVGPSPKFGHAYD 359
 Db 361 GIWIAKTLOPAMETLHASSRHORIODENVYDHTLGLKILNANNEFVGYGVVERNGE 420
 Qy 360 GIWIAKTLOPAMETLHASSRHORIODENVYDHTLGLKILNANNEFVGYGVVERNGE 419
 Db 421 ERMGTFKTFODSREYKVEYNAVADTLEIINDTIRFQSGSEPPKDTIILEQKRISLPL 480
 Qy 420 ERMGTFKTFODSREYKVEYNAVADTLEIINDTIRFQSGSEPPKDTIILEQKRISLPL 479
 Db 481 YSILSALTILGIMASAFLEFNIRKRNOKLIKMSPPYNNLLILGMLSYASIFLFGIDG 540
 Qy 480 YSILSALTILGIMASAFLEFNIRKRNOKLIKMSPPYNNLLILGMLSYASIFLFGIDG 539
 Db 541 GSPSEKTEFTLCTVRWTLVGYTAFSGAMFAKTWRVHAIFKNVKKKKIKDKLLVY 600
 Qy 540 GSPSEKTEFTLCTVRWTLVGYTAFSGAMFAKTWRVHAIFKNVKKKKIKDKLLVY 599
 Db 601 VGMILLIDCILLICQWAVDELRTVERYSMEPPDPAGRDISIRPLEGENTHMTIMGLIV 660
 Qy 600 VGMILLIDCILLICQWAVDELRTVERYSMEPPDPAGRDISIRPLEGENTHMTIMGLIV 659
 Db 661 YAYKGLMLFEGCFIAMETRVNSIPALNSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 720
 Qy 660 YAYKGLMLFEGCFIAMETRVNSIPALNSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 719
 Db 721 CIYALVLIIFCSTLTLCLVEFVPLILTKTNPDAONRFOFTONOKKEDSKTSTVSYN 780
 Qy 720 CIYALVLIIFCSTLTLCLVEFVPLILTKTNPDAONRFOFTONOKKEDSKTSTVSYN 779
 Db 781 QASTSRLEGQSNHRLRKITELDKDLEETMLODOPPEKTYIKONHGOELNDLSIG 840

OY 780 NQASTRLGLOSENHRRLMKITELDKLEBYTMOLODPREKTYIKONHYOELNDLSL 839
 Db 841 GNFTSTDEGKALKNNLNDONPOLOMNTTEPRTCKPDIEDINSPEHIOFRLSLQPLILH 900
 OY 840 GNFTSTDEGKALKNNLNDONPOLOMNTTEPRTCKPDIEDINSPEHIOFRLSLQPLILH 899
 Db 901 HATLPSIGVDASVSPVSPASPRHRHPPSPRVWVSGI 941
 OY 900 HATLPSIGVDASVSPVSPASPRHRHPPSPRVWVSGI 940

RESULT 3
 ID OY133 PRELIMINARY; PRT: 1221 AA.

AC OY133:
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
 DE BCDNA.GH07312.
 GN BCDNA.GH07312.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyroidea; Drosophilidae; Drosophila.

RN [1]
 RP SOURCE FROM N.A.
 RA RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,
 RA AGARWAL A., ARACINA T.J., BAXTER E., BLAZEK R.G., BUTENHOFF C.,
 RA CHAMBERLAIN M., CHAVEZ C., CHEW M., DOYLE C.M., FARFAN D.E., FRISSE E.,
 RA GALLE R., GEORGE R.A., HARRIS N.E., HOSKINS R.A., EVANS-HOLM M.,
 RA HOUTON K.A., HUMASRI S.R., KIM E., LI P., MOSHEE M., PACER J.M.,
 RA PARK S., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T.,
 RA CELINKER S.E.;
 RT "Full length Drosophila melanogaster cDNA sequence."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF145639; RAND38614.1;
 SQ SEQUENCE 1221 AA: 138124 MW: CE3B7865 CRC32;

Query Match 32.3%; Score 2234; DB 5; Length 1221;
 Best Local Similarity 41.5%; Pred. No. 0.00e+00;
 Matches 323; Conservative 195; Mismatches 239; Indels 21; Gaps 17;

Db 18 MSTAAGCTARSD-VYIAGFPFGDGVNSYSGVMPVSKLALGHNEHGKILANTRLH 76
 OY 41 WTGAPRRPSSPPLSLMGLMPLTKEVAKSGRGVLAVALAIDQIRNS-LIRPFLD 99
 Db 77 MMTNDTQCNAAVGVKSPFDMHSGPNKWLFGACTHTVDPIAKSKHMLTQLSVADH 136
 OY 100 LRLDTECDNAKGLKAFDAIKYGNHMLVFGVCPSTSIASLQGMNLVOLFSAAT 159
 Db 137 PMET-KDAPNFRVAVSENAENAPRLALKEFNMTRVGTAYONBPRSLPHNHVADLD 195
 OY 160 PVLADKKKKYFFRYPSDANVAPALIKLKHFRMRVGTILQDVORFSEVRNDLGVLY 219
 Db 196 AMEEVETQSFVNDVAESLKLRENDVAILIGNENEPKAKACEAKLDMYRAQWL 255
 OY 220 GEDLEIDTSEFSDNDPCTSVKTKLKGVDVRIILGFDQNNAAKVCCEAESMFSKQWI 279
 Db 256 IMATYSTDWN-V-TQ-DSE-CSEIEIATLGAALVLDLPLTSGDITAGITADELY 311
 OY 280 IPGVYEPAMWEGYHVEANSSRLRSLLAAMEGYIGVDFEPLSSQKITISGKTPQYER 339
 Db 312 EYDLR-GTEYSRFGHTYDGLWA-A-AL-V-AIOYV-AEKREDLLTHEDYVKNMESVEL 365
 OY 340 EYNSKRGVGPGRKGYAIDGIVAKTLQRMETLHASSRQRIQDPNTYDHTLGLKIL 399
 Db 366 EALNTESEGVGTGVPREYNNERRKANILLNQFOLGMEKIGEXHSOKSLDLSLCKPVKW 425
 OY 400 NAMEETNEFVGQVAFRNGERMGITIKTFQFODSREVKAGEVNAADLEI-INDTRFQ 458
 Db 426 GKTPKXRTILYIHSOVNPTIYASASVIGVIAATVLAFLNFKYNOYITKSSPHL 485
 OY 459 GSPEPKKTIITLBDLRKISLPLISLITSLALTILCMAMASFLFNNKNNQNLIMSSPYM 518

Db 486 NNIIIVGCMMYTLSTIFIGLDTTSSVAAPYICTARANTIMAGFSLSGAMFSTKRVH 545
 OY 519 NNIIIGGLSTASIFLFDGDSFVSGETETCTVTRVTLVYGTAGAAFAATRVH 578
 Db 546 SIFDTLKKRKIKYQOLFVAVGLAIDAIITWQIADPFYRETKODEPLHBNID-D 604
 OY 579 AIFKNVKKMKIKIKQKLLVIVGMLIDICILICWAVDPL-RFTVERYSMEPPAGHD 637
 Db 605 VLVIPNENCOSEHNTIVSITVAYKGLLVFGAFIAMERHVSIFALNDSHIGESYVH 664
 OY 638 ISTRPLEHCENTHMTWLGIVAYKGLMFGCFIAMETRWVSIPALDSKTYIGASVYN 697
 Db 665 VFTICAGAAISLVSDKDLVFLVLSFFIIFCTATLCLVFPKLVLEKRPQGV-DK 723
 OY 698 VGIICITGAASFLTRDQPNVQFCIVALVITFCSTILCLVFPKILTRTNPDAATNR 757
 Db 724 RVATLRPKSKGRDSSVCELEQ----RLDYNNTKCRKRLAMKEKEDLALIRKL 777
 OY 758 RFOFTONKEDSKTISTVSYNQASTSRLEGLOSENHRRLMKITELDKLEBYTMOLO 815

RESULT 4
 ID OY6022 PRELIMINARY; PRT: 844 AA.

AC OY6022:
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, last annotation update)
 DE GABAB RECEPTOR, SUBUNIT 1B, PRECURSOR.
 GN GABAB-R1 OR GABA-B R1B OR GABBR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.

RN [1]
 RP SOURCE FROM N.A.
 RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,
 RA BARNES A.A., EMSON P., POORD S.M., MARSHALL F.H.,
 RT "Heterodimerisation is required to form a functional GABAB receptor."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SOURCE FROM N.A.
 RA KRAUPPANN K., SCHULDER V., MOSBACHER J., BISCHOFF S., BITTGER H.,
 RA HEID J., FROESTL W., LEONHARD S., PRAPF T., KARSGH J.A., BETTER B.,
 RT "Human gamma aminobutyric acid type B receptors are differentially
 expressed and regulate inwardly rectifying K⁺ channels."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).

RN [3]
 RP SOURCE FROM N.A.
 RA YOUNGER R.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ012186; CAA09940.1;
 DR EMBL: AJ225029; CAA12360.1;
 DR EMBL: AL031983; CAA21454.1;
 KW Signal; Receptor.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 844 GABAB RECEPTOR, SUBUNIT 1B.
 SQ SEQUENCE 844 AA: 95148 MW: C7342B77 CRC32;

Query Match 24.4%; Score 1684; DB 4; Length 844;
 Best Local Similarity 35.3%; Pred. No. 0.00e+00;
 Matches 254; Conservative 191; Mismatches 255; Indels 19; Gaps 17;

Db 40 SRVDPHSSERRAVYTGALFPMVS-G-GMPG-GQACQPAVEMALFDVNSRDILPYELKL 96
 OY 42 TRGAPRRPSSPPLSLMGLMPLTKEVAKSGRGVLAVALAIDQIRNE-SLRPFLD 100
 Db 97 IHDSCDPCQATKYLYELLYNDPIKILIMP-G-CSSVTLVAEARMNLIYSGSSSP 155
 OY 101 RLVTEDCNKGLKAFDAIKYGNHMLVFGVCPSTSIASLQGMNLVOLFSAATRP 160
 Db 156 ALSNRQRFPTFFPTHPASLHNPTRVKKLFERKMGKIKATIQGTIEVFTSLDLEBRVNE 215

QY	75	GVLPAAVELAQEIRNE-SLAPFLYDLRLVDTBCDNAAKGLAAFYDAIKYGNHLMVEGV	133
Db	129	CSSVSTLVLAFAARMNLLVLSYSSSSPALSNRORPEPTFRPSATLHNPRLYLFKMG	168
QY	134	GPSTVSTLHESLQGNLQVLSFPAATLYLADKKRIYFRTYPSDNNAYPALTLKLFHR	193
Db	189	WKRIATIQGTTEVTSTUDDLEERVKAGIEITFRQSPFSDAVPVKNLKKODARITVGL	248
QY	194	WRERVGLTLDVDFEVEFVENDTLGVLYEDEIDIESDTEFSNDCTSYKKLKNDRVLLTQ	253
Db	249	FYTEERKRFCEVYKERLFGKKYVFLICGYAANWV-KTY-PP-SINCTVEGMTAEVGH	305
QY	254	PDQNNAAKVFCCAFEDSFSGSKYMIIPGYEPAMWQYHVAANSRCLRRSLAABGY	313
Db	306	ITTEIYMLNPAMTBRSISMVSOEFVEKLTRLKRHEDEFGQDEAPLAYDAIMLALAN	365
QY	314	IGVDEPFLSSKOIKITISCKTPOQI-EHEVNS-KRSGVGSKEH-G-YAIDGIMVIAKTLO	369
Db	366	KTSGG--GGRSGVLEDDENYNNQITIDQIYRANSSSEFVSGHYVFDASGRMAWTLIE	423
QY	370	RAEETHASSRQRRIODPNYNDHTLGLILNANNENFEGVYGQVVF-RNGBRGGITKFT	428
Db	424	QLQGGYKIKIYSDTRKDLNW-SKTEPKWIGSGPPADQTLVTKTFRPLISOKLITISVLS	482
QY	429	QPDSEKVEKGYENNAVTLTLLINDTIRFGSGSEPPDKTILIEQLKRLSLPGLTSLMT	488
Db	483	SLGIVTAVVCSFNTYNSHVARYTONSOPNUNNTAVGCSLAAAVFPLGIDGTHIGRSQF	542
QY	489	ILDMIASAFLEFNKRNKNOQLIKMSSPPYNNMLILIGMISYASISFLTGLDGSPVSEKTF	548
Db	543	PVYQCARWLMLLGLGSLGSGMFTKIMWHTVETFKERKEKRLLEPMKLYATVGLLVG	602
QY	549	ETICTRTYRLITVGTATFAFGMAFKTRVHAIE--KNVKKK-KKIIKOKLTVIYGKLL	605
Db	603	MDVLTATMOIYDPLHRTIEFFAKEEKEDIVSIIIPOLHSGSKMNTWLGIFYGKGL	662
QY	606	IDCILICLQMDAPDLKRIYERYSMEPPPARDOISIRPLDEHCENHMTWLGITYAKGL	665
Db	663	LILGLFLAETFKSYSTEKINDHAGMAIYNAVLCITAPYTMILSSQDAAFAPARSL	722
QY	666	LMFGEFLMERNRNSISALNDSKYIDGMSYVNGIMCIIIGAAVSFLTRDOPNOFCIVAL	725
Db	723	AIYESSITLVLPYKMRRLITRGE 748	
QY	726	VIIFCSTITCLVFPVKILITRTMPD 751	
RESULT	6	PRELIMINARY: PRT; 833 AA.	
ID	03WV15;		
AC	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	573K1.1.4 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1D).		
EN	573K1.1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	YOUNGER R.		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL078630; CAB44993.1; -.		
KW	Receptor.		
SO	SEQUENCE 833 AA; 93167 MW; 0C07A359 CRC32;		
Query Match	24.3%;	Score 1681; DB 11;	Length 833;
Best local Similarity	35.1%;	Pred. No. 0+0er+0;	
Matches	262;	Conservative 192;	Mismatches 269; Indels 23; Gaps 21.
Db	13	PURLIYMAAGYAPWASHSP-HLPRHPRVPRHPSERRAYTGL-FPMSCGPG-GQ	69
QY	19	PARLLPULISLI-LWLAFGWGMWTRQAPR-PP-PSSPPLST-MGLMPTREKVAAGSTGR	74

Qy 724 ALVIFCSITITCLVFPKLTITKTNPD 751

RESULT 10
ID 095375 PRELIMINARY; PRT: 961 AA.

AC 095375;
DT 01-MAY-1999 (Tremblrel, 10, Created)
DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel, 12, Last annotation update)
DE GABA-B1A RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

RA STRONG U. RAMING K.
RT "Human mRNA for GABA-B1a receptor."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF099148; AAC9508.1; -
DR HSSP: P10998; IYVC.
KW Receptor.
SQ SEQUENCE 961 AA; 108336 MW; 14545CBE CRC32;

Query Match 24.3%; Score 1676; DB 4; Length 961;
Best local similarity 36.0%; Pred. No. 0.00e+00;
Matches 248; Conservative 179; Mismatches 245; Indels 16; Gaps 14;

Db 185 GACACPAVMALEEDVNSRRDIPDYELKLHDSKCDPGATKYLYELLNDPKITLMP 244
Qy 73 GRCVLPVAVLALAEQIRNE-SLRPFYDLRLYTECDNAGLAFYDAIKYGNHLMVFG 131
Db 245 G-CSSVSTLVAAARMWNLIVSYGSSPALSNRPFRTFTHPSATLHNPTRVLFEEK 303
Qy 132 GVCPSVSTIAISLQGMNLYOLSFATTPVLADKKKPYFFRTVPSDMANPRILKLKH 191
Db 304 WKKKATATQOQTEVFTSLDLERYKAEIETTFROSFPSPAPVYKLNQDARIIV 363
Qy 192 FRRRRGITLQVORSEVRNDLTVLGEDIEISDSESNPCISYKTKKGNDRITL 251
Db 364 GLFYEETARKVCEVYKKEFLGKYVFLIGVADNMF-KIY-DP-SINCTVDEMTAVE 420
Qy 252 GQPDQMAKAVCCAFEESEMGSKYQWIIIPGWPAMWQVHYEANSRRLRSLLAAWE 311
Db 421 GHTTTEIVLNPANTRISNMTSOFVFKLTKRKHPDEETGQEPAPLAYDAIALALA 480
Qy 312 GYIGVDFEPLSSKQIKTISGKTPQY-BREYNS-KRSGVPSKFH-G-YAIDGIWIAKT 367
Db 481 LNKTSGG--GGRSGVLEDFNNQITTDQIYRAMNSSSEFGVSGHYVDPASGRAMTL 538
Qy 368 LQRAMETLHASSRHQIDQFNHTDHLTKILNMANETNFGVGVYF-RNGERMGTIK 426
Db 539 IEOLQGSYKKIKGYDSTKDDLSW-SKTDKMTGSPAPDQIYKTRFISQKLFSTISGV 597
Qy 427 FTQFQDSREYKGEINAVADTLEIINDIRIOGSEPPKDKITLQKRSKISLPSYILSA 486
Db 598 LSSSLGIYLVAVCLSFNIYNSHVRIYNSOPNLNLTAVGSLAAVPLGLDGYHGRN 657
Qy 487 LTLIGIMASAFLEFNKIKRNOKLIKMSPPYNNLILIGWLSYASIFLGLDGSFVSEK 546
Db 658 OPFVCOARWMLGLGFSLGYSMTKIMWVHYVTFKKEEKERKLTLEPMKLYAVGSL 717
Qy 547 TFEFLTVRMIWLYGTTFYAFGAMFAKTRVNAIF-KNVMK-KTIIRKQKLLIVYGGM 603
Db 718 VGMDVLTALAIQVLDLHRTIETFAKEPKREDIVSLIPOLHSSSKRMNTWLGIFYGX 777
Qy 604 LLLDLCLILCMQAVDPLRTRVERYSMEPPAGRODISIRPLEHEENHMTWIGIYAYX 663
Db 778 GLLLLGLIYLETTSKSTKINDIRAVGMAIYNAVCLITTAQVMTILSQQDAFAFA 837
Qy 664 GLMLTECFIAMEITRNVSTIPALNDSKYSIMSYNGIMCIIGAVSVLTLDQDPVQFCIV 723
Db 838 SLAIVSSYITLVVLFVPMKRLITRGE 865

Qy 724 ALVIFCSITITCLVFPKLTITKTNPD 751

RESULT 11
ID 095468 PRELIMINARY; PRT: 930 AA.

AC 095468;
DT 01-MAY-1999 (Tremblrel, 10, Created)
DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel, 12, Last annotation update)
DE GABABRI PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

RA PETERS H.C., KAEMER G., VOZ A., KAUPMANN K., ZIEGLER A., BETTLER B.,
RT "Mapping, genomic structure and polymorphisms of the human gababrl
RT receptor gene: evaluation of its involvement in idiopathic generalized
RT epilepsy."
RL Neurogenetics 2:47-54(1998).

DR EMBL: AJ010170; CAA09031.1; JOINED.
DR EMBL: AJ010171; CAA09031.1; JOINED.
DR EMBL: AJ010172; CAA09031.1; JOINED.
DR EMBL: AJ010173; CAA09031.1; JOINED.
DR EMBL: AJ010174; CAA09031.1; JOINED.
DR EMBL: AJ010175; CAA09031.1; JOINED.
DR EMBL: AJ010176; CAA09031.1; JOINED.
DR EMBL: AJ010177; CAA09031.1; JOINED.
DR EMBL: AJ010178; CAA09031.1; JOINED.
DR EMBL: AJ010180; CAA09031.1; JOINED.
DR EMBL: AJ010181; CAA09031.1; JOINED.
DR EMBL: AJ010182; CAA09031.1; JOINED.
DR EMBL: AJ010183; CAA09031.1; JOINED.
DR EMBL: AJ010184; CAA09031.1; JOINED.
DR EMBL: AJ010185; CAA09031.1; JOINED.
DR EMBL: AJ010186; CAA09031.1; JOINED.
DR EMBL: AJ010187; CAA09031.1; JOINED.
DR EMBL: AJ010188; CAA09031.1; JOINED.
DR EMBL: AJ010189; CAA09031.1; JOINED.
DR EMBL: AJ010190; CAA09031.1; JOINED.
DR EMBL: AJ010191; CAA09031.1; JOINED.
DR HSSP: P10998; IYVC.
SQ SEQUENCE 930 AA; 104564 MW; B825E4F7 CRC32;

Query Match 24.2%; Score 1671; DB 4; Length 930;
Best local similarity 36.0%; Pred. No. 0.00e+00;
Matches 248; Conservative 180; Mismatches 243; Indels 17; Gaps 15;

Db 185 GACACPAVMALEEDVNSRRDIPDYELKLHDSKCDPGATKYLYELLNDPKITLMP 244
Qy 73 GRCVLPVAVLALAEQIRNE-SLRPFYDLRLYTECDNAGLAFYDAIKYGNHLMVFG 131
Db 245 G-CSSVSTLVAAARMWNLIVSYGSSPALSNRPFRTFTHPSATLHNPTRVLFEEK 303
Qy 132 GVCPSVSTIAISLQGMNLYOLSFATTPVLADKKKPYFFRTVPSDMANPRILKLKH 191
Db 304 WKKKATATQOQTEVFTSLDLERYKAEIETTFROSFPSPAPVYKLNQDARIIV 362
Qy 192 FRRRRGITLQVORSEVRNDLTVLGEDIEISDSESNPCISYKTKKGNDRITL 251
Db 364 GLFYEETARKVCEVYKKEFLGKYVFLIGVADNMF-KIY-DP-SINCTVDEMTAVE 419
Qy 252 GQPDQMAKAVCCAFEESEMGSKYQWIIIPGWPAMWQVHYEANSRRLRSLLAAWE 311
Db 420 GHTTTEIVLNPANTRISNMTSOFVFKLTKRKHPDEETGQEPAPLAYDAIALALA 479
Qy 312 GYIGVDFEPLSSKQIKTISGKTPQY-BREYNS-KRSGVPSKFH-G-YAIDGIWIAKT 367
Db 480 LNKTSGG--GGRSGVLEDFNNQITTDQIYRAMNSSSEFGVSGHYVDPASGRAMTL 537

OY 733 ITLCVFEVKLITLRTNPDATONRRFOFONOKKEDSKTSTSVYNQASTSRLEGLOS 792
Db 61 ENHRLRMKITEIDKDLDEEVTMOLODTPERTTYIKONHYOELNDILNIGNFTSTGGKAI 120
OY 793 ENHRLRMKITEIDKDLDEEVTMOLODTPERTTYIKONHYOELNDILNIGNFTSTGGKAI 852
Db 121 LKNHLDONPOLQWNTTSPSRICKDPIEDINSBERTIORRLSLQPLHAYLPSTIGVDAS 180
OY 853 LKNHLDONPOLQWNTTSPSRICKDPIEDINSBERTIORRLSLQPLHAYLPSTIGVDAS 912
Db 181 CVSPCVSPTASPRHR 195
OY 913 CVSPCVSPTASPRHR 927

Search completed: Wed Mar 15 22:31:19 2000
Job time : 1040 secs.

 W E R E L F

 (TM)

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Merch_LDP protein - protein database search, using Smith-Waterman algorithm
 Run on: Wed Mar 15 22:06:55 2000; MasPar time 38.30 Seconds
 Tabular output not generated. 733.025 Million cell updates/sec

Title: >US-09-211-755-4
 Description: (1-940) from US09211755.pep
 Perfect Score: 6906
 Sequence: 1 MASPPSSGQPRPPPPPPPPA.....TASPRHRVPPSPFVYVMSGL 940

Scoring table:
 Gap 11
 PAM 150

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 56.654; Variance 109.020; scale 0.520

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	240	3.5	908	1	MGR8_MOUSE	2.21e-20
2	236	3.4	871	1	MGR6_RAT	1.10e-19
3	236	3.4	908	1	MGR8_RAT	1.10e-19
4	232	3.4	908	1	MGR6_HUMAN	5.44e-19
5	225	3.3	877	1	MGR6_HUMAN	8.73e-18
6	228	3.3	912	1	MGR4_HUMAN	2.67e-18
7	225	3.3	912	1	MGR4_HUMAN	8.73e-18
8	214	3.1	915	1	MGR7_RAT	6.48e-16
9	214	3.1	915	1	MGR7_HUMAN	6.48e-16
10	215	3.1	1203	1	MGR5_RAT	4.39e-16
11	215	3.1	1212	1	MGR5_HUMAN	4.39e-16
12	210	3.0	976	1	MGR_DROME	3.05e-15
13	199	2.8	1079	1	CASR_RAT	2.04e-13
14	193	2.8	872	1	MGR2_HUMAN	1.95e-12
15	194	2.8	1078	1	CASR_HUMAN	1.34e-12
16	182	2.8	1085	1	CASR_BOVIN	2.84e-12
17	186	2.7	872	1	MGR2_RAT	2.64e-11
18	188	2.7	877	1	MGR3_HUMAN	1.26e-11
19	188	2.7	879	1	MGR3_RAT	1.26e-11
20	178	2.6	1194	1	MGR1_HUMAN	4.91e-10
21	178	2.6	1199	1	MGR1_RAT	4.91e-10
22	164	2.4	986	1	CYGR_ARBP	7.16e-08
23	165	2.4	1108	1	CYGF_RAT	5.05e-08

RESULT ID	1	STANDARD	PRT	908 AA	ALIGNMENTS
AC	MGR8_MOUSE				
AC	P47743				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	15-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.				
GN	GRM8 OR MGLUR8.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6; TISSUE=RETINA;				
RX	MEDLINE: 95239344;				
RA	DUVOISIN R.M., ZHANG C., RAMONDEL K.;				
RT	"A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb."				
RT	J. Neurosci. 15:3075-3083(1995).				
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB, ACCESSORY OLFACTORY BULB, AND MAMMARY BODY. WEAKER EXPRESSION IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDRAIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL: U17252; AAA68149.1; -				
DR	GCDB: GCR.1712; -				
DR	MCD: MGT.109600; GRM8				
DR	PROSITE: PS00979; G-PROTEIN_RECP_F3_1; 1.				
DR	PROSITE: PS00980; G-PROTEIN_RECP_F3_2; 1.				
DR	PROSITE: PS00981; G-PROTEIN_RECP_F3_3; 1.				
DR	PFAM: PF00003; 7tm_3; 1.				
DR	PFAM: PF01094; ANF_receptor; 1.				
KM	G-protein coupled receptor; Transmembrane; Glycoprotein; signal;				
KM	Multigene family; Olfaction.				
FT	SIGNAL 1 33				

	CC	-I-	TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR LAYER OF THE RETINA.
	CC	-I-	SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
	CC		STRONGEST: TO MDIUR4.
	CC		-----
	CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
	CC		-----
	DR	EMBL:	DJ3963; BAA03066.1; .
	DR	PIR:	A46742; A46742.
	DR	GCRDB:	GCR_0623; .
	DR	PROSITE:	PS00979; G_PROTEIN_RECPE_F3_1; 1.
	DR	PROSITE:	PS00980; G_PROTEIN_RECPE_F3_2; 1.
	DR	PROSITE:	PS00981; G_PROTEIN_RECPE_F3_3; 1.
	DR	PFAM:	PF00003; 7tm_3; 1.
	DR	PFAM:	PF01094; ANF_receptor; 1.
	KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;	
	KW	Multigene family; Vision.	
	FT	SIGNAL	1
	FT	CHAIN	18
	FT	DOMAIN	19 871 METABOTROPIC GLUTAMATE RECEPTOR 6.
	FT	TRANSSEM	19 579 EXTRACELLULAR (POTENTIAL).
	FT	TRANSSEM	580 602 I (POTENTIAL).
	FT	DOMAIN	603 616 CYTOPLASMIC (POTENTIAL).
	FT	TRANSSEM	617 637 II (POTENTIAL).
	FT	DOMAIN	638 648 EXTRACELLULAR (POTENTIAL).
	FT	TRANSSEM	649 667 III (POTENTIAL).
	FT	DOMAIN	668 691 CYTOPLASMIC (POTENTIAL).
	FT	TRANSSEM	692 712 IV (POTENTIAL).
	FT	DOMAIN	713 742 EXTRACELLULAR (POTENTIAL).
	FT	TRANSSEM	743 764 V (POTENTIAL).
	FT	DOMAIN	765 777 VI (CYTOPLASMIC (POTENTIAL)).
	FT	TRANSSEM	778 800 VII (POTENTIAL).
	FT	DOMAIN	801 813 EXTRACELLULAR (POTENTIAL).
	FT	TRANSSEM	814 839 VIII (POTENTIAL).
	FT	DOMAIN	840 871 CYTOPLASMIC (POTENTIAL).
	FT	CARBOHYD	290 290 POTENTIAL.
	FT	CARBOHYD	445 445 POTENTIAL.
	FT	CARBOHYD	473 473 POTENTIAL.
	FT	CARBOHYD	561 561 POTENTIAL.
	SQ	SEQUENCE	871 AA; 95089 MW; 81A229E4 CRC32;
		Query Match	3.4%; Score 236; DB 1; Length 871;
		Best Local Similarity	22.9%; Pred. No. 1.0e-19;
		Matches	64; Conservative 90; Mismatches 102; Indels 24; Gaps 21;
	Db	586 LAVIG-I-MATTIMATPMKNDPTIVRASGRELSTYLITGIFLITA-T-TF-L--MYAE	638
	Oy	LTIIGMIMASAPLEFFIKNRNK-LIKSSPYNNKLIIIGMSYASIFLPGLDSPFE	545
	Db	639 PC-AALCAARLLIGTLISALTETKNYVIFEQGRSVTPPPFIISPQSOLVITFG	697
	Oy	KTFELICTAYRWILAVGYTTAFGAFAKTVAHIFKNX--MKK-IKDOKLVIWG	602
	Db	698 LTSOVGVYIAMIGNOPHSVID-E-QQRVDEQA-RGVTK-COMSLST-IGCL-GY	751
	Oy	MLIDLCILCMOWDPLRYVERKSMEPDAGDISIRPLEHCENTMTIMLGIVAY	662
	Db	752 -SILLMWTC-TVYAIAKRGVPETFEANAPDIGFTMYTTCIIIMAFVIPFGTAQSAEKIYI	809
	Oy	KGLIMTFGCFLAMEFNNSIP-ALNDSKYISMYSYANGVICIIIGAASFPLTDOPNOFC	721
	Db	810 QTTLVTSLSASVISGLMYPKYYVLFPEDVOGKRK	849
	Oy	722 -IVALVI-I-FCSITILCLVFYPKILITLRTPDAATONRR	758
	RESULT	3	
	ID	MGR8_RAT	STANDARD: PRT: 908 AA.

AC P70579;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
 GN GRM8 OR MGLUR8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97168760.
 RA SAUGSTAD J.A., KINZIE J.M., SHINOHARA M.M., SEGGERSON T.P.,
 RA WESTBROOK G.L.;
 RA "Cloning and expression of rat metabotropic glutamate receptor 8
 RT reveals a distinct pharmacological profile."
 RL Mol. Pharmacol. 51:119-125(1997).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
 CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
 CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
 CC HIPPOCAMPUS, CEREBELLUM, AND MAMMARY BODY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U63288; AAB09537.1; -.
 DR GCRDB; GCR_1411; -.
 DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PFM; PF00003; 7tm_3; 1.
 DR PFM; PF01094; ANF_receptor; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Olfaction.
 FT SIGNAL 1 33
 FT CHAIN 34 908
 FT DOMAIN 34 583
 FT TRANSMEM 584 608
 FT DOMAIN 609 620
 FT TRANSMEM 621 641
 FT DOMAIN 642 647
 FT TRANSMEM 648 668
 FT DOMAIN 669 695
 FT TRANSMEM 696 716
 FT DOMAIN 717 746
 FT TRANSMEM 747 768
 FT DOMAIN 769 781
 FT TRANSMEM 782 803
 FT DOMAIN 804 818
 FT TRANSMEM 819 843
 FT DOMAIN 844 908
 FT CARBOHYD 95 95
 FT CARBOHYD 298 298
 FT CARBOHYD 452 452
 FT CARBOHYD 480 480
 FT CARBOHYD 565 565
 SQ SEQUENCE 908 AA; 101866 MW; 5043FE81 CRC32;
 Query Match 3.4%; Score 236; DB 1; Length 908;
 Best Local Similarity 21.9%; Pred. No. 1,10E-19;
 Matches 62; Conservative 97; Mismatches 100; Indels 24; Gaps 21;

QY 487 ILIICIMASAFLEFN-IKNRNOKLIKNSSPYNNLLILGMSYASIFLEGDGSPVSE 545
 Db 645 -TI-ICSEFRIFLIGLGCFSYALITKTRIRHIFEGGKSYAPKIFISASOLVTFPS 701
 QY 546 KTFEFLCTVRITLVGTITTFGAFNAFTWYHAFKRVKAK-K-KIINDOKLLVIVGG 602
 Db 702 LISVOLLGVFWFVVDPPHTIID-YG-DORTLDE-NARGVLK-CDISDSL-ICSL-GY 755
 QY 663 KGLMLFGCFLAMETRNNSIP-ALNDSKYIGMSYVNGVICIIGAASFLTRDPNVOFC 721
 Db 814 QTTTLVSMSLSASVSLGMLWPKYIIIFHEQNVQKRKSF 856
 QY 722 -IVALVT-I-FCSTITLCLVFPKILITLRNDATQNRROF 761
 RESULT 4
 ID MGR8 HUMAN STANDARD; PRT; 908 AA.
 AC 000222; 015493;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
 GN GRM8 OR MGLUR8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98141892.
 RA WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
 RA ROSTOP P.R. JR., JOHNSON B.G., SCHORPP D.D., BELGAJE R.M.;
 RT Group III human metabotropic glutamate receptors 4, 7 and 8:
 RT molecular cloning, functional expression, and comparison of
 RT pharmacological properties in RGT cells."
 RL Brain Res. Mol. Brain Res. 53:88-97(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97446143.
 RA SCHERER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.;
 RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
 RT disproportionately large gene located at 7q31.3-q32.1."
 RL Genomics 44:232-236(1997).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U92459; AAB51764.1; -.
 DR EMBL; U95025; AAB72040.1; -.
 DR GCRDB; GCR_1889; -.
 DR GCRDB; GCR_2604; -.
 DR MIM; 601116; -.
 DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PFM; PF00003; 7tm_3; 1.
 DR PFM; PF01094; ANF_receptor; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Olfaction.

```
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
FT CONFLICT 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 N -> I (IN REF. 2).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA; 101741 MW; 188650CF CRC32;
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Query Match 3.4%; Score 232; DB 1; Length 908;
Best Local Similarity 23.0%; Pred. No. 5,44e-19;

Matches 65; Conservative 96; Mismatches 98; Indels 24; Gaps 21;

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Db 590 VALGII-ATFEVIVFVRNDPIVRASGRELSTYLLGLGIFLCSITFLM-I-AA--PD 644
Qy 487 LTLIGMIMASAFLEFN-INKRNOKLIKMSPPYNNMLIIIGMLSVASIFLFDLDSFVSE 545
Db 645 -T-TCSEFRVFLGMCFSYALLTKNRHIFEGQKSVYAPKFTSPASQLVITFS 701
Qy 546 KTFETCTVFTWLVGYTTAFGAMFAKTWRVHAIFKNYKMK-K--KIHKDKLIVYGG 602
Db 702 LISVQLGVEVFWVDDPHIID-YG-EORTLDPEKA-RGVLK-CDISLST-IGSL-GY 755
Qy 603 MLIDLCILICQAVDPLRRTVERYSMEPDPAGRDISIRPLEHECHNTMTIWLGIYAY 662
Db 756 SILLMW-TCTVYANKTRGV-ETENEAKPIGFTMTTCIIMLAFPIFGTAQSAEKYI 813
Qy 663 KGLMFGCFL-AMETRNYSIPALNDSKYIGSVYVNGIMCIIGAASFLTRDQPNVQFC 721
Db 814 OTTLVVSLSASVSLGMLYPKYIIIFHPEQNVQKRKSF 856
Qy 722 -IYALVI-I-FCSTITLCLVFPVKLTITLTPDAATQNNRRQF 761
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RESULT 5
AC MGR6 HUMAN STANDARD. PRT; 877 AA.
AC 015303:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR MGLUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97358610.
RA HASHIMOTO T., INAZAWA J., OKAMOTO N., TAGAMA Y., BESSHO Y., HONDA Y.,
RA NAKANISHI S.;
RT "The whole nucleotide sequence and chromosomal localization of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).
```

```
CC -I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC ACTIVITY.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: U82083; AAB82068.1; -.
DR GCRDB: GCR_2607; -.
DR MIM: 604096; -.
DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PRAM: PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 24
FT CHAIN 25 877 POTENTIAL.
FT DOMAIN 25 585 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 586 608 I (POTENTIAL).
FT DOMAIN 609 622 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 623 643 II (POTENTIAL).
FT DOMAIN 644 654 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 655 673 III (POTENTIAL).
FT DOMAIN 674 697 IV (POTENTIAL).
FT TRANSSEM 698 718 V (POTENTIAL).
FT DOMAIN 719 748 VI (POTENTIAL).
FT TRANSSEM 749 770 VII (POTENTIAL).
FT DOMAIN 771 783 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 784 806 VI (POTENTIAL).
FT DOMAIN 807 819 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 820 845 VII (POTENTIAL).
FT DOMAIN 846 877 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 877 877 POTENTIAL.
FT CARBOHYD 926 926 POTENTIAL.
FT CARBOHYD 451 451 POTENTIAL.
FT CARBOHYD 479 479 POTENTIAL.
FT CARBOHYD 567 567 POTENTIAL.
SQ SEQUENCE 877 AA; 95436 MW; D5A6C038 CRC32;
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Query Match 3.3%; Score 225; DB 1; Length 877;
Best Local Similarity 21.5%; Pred. No. 8,73e-18;
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

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Db 592 LAVLGIVATTIVATVVRNNNPVIRASGRELSTYLLGLIPLIV-I-TF-I--MVAP 645
Qy 487 LTLIGMIMASAFLEFNINKRNOKLIKMSPPYNNMLIIIGMLSVASIFLFDGDSFVSEK 546
Db 646 G-AAVCARRFLGTSTSYSLALTKTRIRYIFEGQKRSVTPPPSPISQVITTSI 704
Qy 547 TFEETLCTVFTWLVGYTTAFGAMFAKTWRVHAIFKNYK--MKK-IHKDKLIVYGG 603
Db 705 TSLQVVGMTAMTGARPHSVID-YE-EORTVDEQA-RGVLK-CDMSLST-IGCL-GY- 757
Qy 604 LTLIDLCILICQAVDPLRRTVERYSMEPDPAGRDISIRPLEHECHNTMTIWLGIYAYK 663
Db 758 SILLMWTC-TYVALKARGVPEFNKAPRIGFTMTTCIIMLAFVPIFGTAQSAEKYIQ 816
Qy 664 GLTMFGCFLAMETRNVSIP-ALNDSKYIGSVYVNGIMCIIGAASFLTRDQPNVQFC- 721
Db 817 TTTLVVSLSASVSLGMLYPKYIIIFHPEQNVQKRKSF 855
Qy 722 IYALVI-I-FCSTITLCLVFPVKLTITLTPDAATQNNRR 758
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FT	DOMAIN	646	656	675	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	657	675	695 <td>II (POTENTIAL).</td>	II (POTENTIAL).
FT	DOMAIN	676	699 <td>720<td>CYTOPLASMIC (POTENTIAL).</td></td>	720 <td>CYTOPLASMIC (POTENTIAL).</td>	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	700	720 <td>750<td>IV (POTENTIAL).</td></td>	750 <td>IV (POTENTIAL).</td>	IV (POTENTIAL).
FT	TRANSSEM	721	750 <td>772<td>EXTRACELLULAR (POTENTIAL).</td></td>	772 <td>EXTRACELLULAR (POTENTIAL).</td>	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	751	772 <td>785<td>V (POTENTIAL).</td></td>	785 <td>V (POTENTIAL).</td>	V (POTENTIAL).
FT	DOMAIN	773	785 <td>808<td>CYTOPLASMIC (POTENTIAL).</td></td>	808 <td>CYTOPLASMIC (POTENTIAL).</td>	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	786	808 <td>821<td>VI (POTENTIAL).</td></td>	821 <td>VI (POTENTIAL).</td>	VI (POTENTIAL).
FT	DOMAIN	809 <td>821<td>847<td>EXTRACELLULAR (POTENTIAL).</td></td></td>	821 <td>847<td>EXTRACELLULAR (POTENTIAL).</td></td>	847 <td>EXTRACELLULAR (POTENTIAL).</td>	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	822	847 <td>912<td>VII (POTENTIAL).</td></td>	912 <td>VII (POTENTIAL).</td>	VII (POTENTIAL).
FT	DOMAIN	848	912 <td>98<td>CYTOPLASMIC (POTENTIAL).</td></td>	98 <td>CYTOPLASMIC (POTENTIAL).</td>	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	98	98 <td>301<td>POTENTIAL.</td></td>	301 <td>POTENTIAL.</td>	POTENTIAL.
FT	CARBOHYD	301	301 <td>454<td>POTENTIAL.</td></td>	454 <td>POTENTIAL.</td>	POTENTIAL.
FT	CARBOHYD	454	454 <td>484<td>POTENTIAL.</td></td>	484 <td>POTENTIAL.</td>	POTENTIAL.
FT	CARBOHYD	484	484 <td>569<td>POTENTIAL.</td></td>	569 <td>POTENTIAL.</td>	POTENTIAL.
FT	CARBOHYD	569	569 <td>912 AA.<td>POTENTIAL.</td></td>	912 AA. <td>POTENTIAL.</td>	POTENTIAL.
SO	SEQUENCE	912 AA. <td>101867 MM.<td>7409054 CRC32.<td></td></td></td>	101867 MM. <td>7409054 CRC32.<td></td></td>	7409054 CRC32. <td></td>	

Query Match	3.38.	Score 228.	DB 1.	Length 912.
Best Local Similarity	21.68.	Pred. No. 2,67e-18.		
Matches	62.	Conservative	98.	Mismatches 100.
				Indels 27.
				Gaps
Db	588	AVLPFLFAVVG-FAATLPEVITPVRYNDPIYKASGRSLSVLGLAIFLCVATPL--M-643		
Qy	482	SILSK-LTILGIMASAFLEFN-IRKNOKILIMSSPNNNLITLGLMSYSLFGLD-539		
Db	644	--INAEIDIGT-CLSRIPILGIGMSIYALAKTNRIYRFEEGGRKSARSPFSPASQ-699		
Qy	540	GSFVSEKTFELLCYVATWLLVGTTFAGMFAKTRVHALFKNV-KKK-KILIKDKL-596		
Db	700	LAIFSLISLQQLGICWFWVDSDSHVD-FODORTLDP-FA-RGVLK-CDISDSL-753		
Qy	597	LTVSGMLLIDLCILIC-WQAVDEPLRFRYERSMDEPDAGDISIRPLEHCENHMTI-655		
Db	754	ICLL-GYSMLAN-TC-TVYAIKTRGVPEFENFARPIGFTYTCIYMLAIFIPFGTSQ-810		
Qy	656	LGIYVAYKGLMLFGGFLAMETRNVSIP-ALNDSKYIKMSYVNGIICGAASFTRD-714		
Db	811	SADKIXIOTTLTVYSUSASYSIGMLYMKXYIILFPEQDNVSKR-857		
Qy	715	QPNVOFC-IYALVI-I-FESTITLCLVFPKLLITLTNPDAATONRR-758		

RESULT	7	STANDARD:	PRT:	912 AA.
ID	MGRA.RAT			
AC	P31423:			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUL-1989 (Rel. 38, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.			
DN	GRM4 OR MEUR4.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NN	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RC	MEDLINE: 92110002.			
RA	TANAE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;			
RT	"A family of metabotropic glutamate receptors."			
RL	Neuron 8:169-179(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RC	MEDLINE: 93332699.			
RA	O'HARA P.D., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B.A.,			
RA	MCGRANE V., HOUWDE K.M., THOMSEN C., GILBERT T.L., MULVIHILL E.R.;			
RT	"The 11and-binding domain in metabotropic glutamate receptors is			
RT	related to bacterial periplasmic binding proteins."			
RL	Neuron 11:41-52(1993).			
CC	-I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR			
CC	IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE			
CC	ACTIVITY.			

FT TRANSMEM 789 810 VI (POTENTIAL).
 FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 826 850 VII (POTENTIAL).
 FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 458 458 POTENTIAL.
 FT CARBOHYD 486 486 POTENTIAL.
 FT CARBOHYD 572 572 POTENTIAL.
 SQ SEQUENCE 915 AA; 102231 MW; AF4AD466 CRC32;

Query Match 3.1%; Score 214; DB 1; Length 915;
 Best Local Similarity 22.9%; Pred. No. 6,48e-16;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

DB 597 LAMGII-ATIFVWATPIRYNDPIYASGRELSTVLTGIFLCY--IIF-L--MIA- 648
 QY 487 LTLIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLILGMLSTASIFLGLDGSFVSE 545
 DB 649 KPDVAVCSFRFVGLGMCISYALTLTKNRIYRIFEOGKRSVTAPRLISPTSLATSS 708
 QY 546 KTEFLICTRWILTVGTTAFGAMFAKTWRVHAIFKNYKMK-K-KIKDOKLVIYVG 602
 DB 709 LISVOLGVEI-WGVDPNIIID-YD-EHKTNPEQA-RGYLK-CDITDLOI-IGSL-G 761
 QY 603 MLTIDL-CILICWQAVDPLRTYRYSMEPDAGDISIRPLEHCENTHTATWLGIVYA 661
 DB 762 YSILIMV-TC-TVYAIKTRGVENENKAPIGFTMTTCIYWLAFIPFEGTAOSAKELY 819
 QY 662 YKGLMLFEGCLAMETRNVSIPA-LNDSKRYIGMSYVNGIMCIIGAAVSFLTRDOPWOF 720
 DB 820 IOTTLTISMLNSASVALGMLYMPKVIIFHELVNOKRKSF 863
 QY 721 C-IVALVI-I-FCSTITLCLVFPKLTITLTPNDATONRRROF 761

RESULT 9
 ID MGR7_HUMAN STANDARD; PRT; 915 AA.
 AC Q14831;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
 GN GRM7 OR MGLUR7.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 96437220.
 RA MAKOFF A., PILLING C., HARRINGTON K., EMSON P.;
 RT "human metabotropic glutamate receptor type 7: molecular cloning and
 mRNA distribution in the CNS.";
 RL Brain Res. Mol. Brain Res. 40:165-170(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98141892.
 RA WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
 RA ROSECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELGAUD R.M.;
 RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
 molecular cloning, functional expression, and comparison of
 pharmacological properties in RGT cells";
 RL Brain Res. Mol. Brain Res. 53:88-97(1998).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST TO MGLUR4.
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 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL; X94552; CA64245.1; -
 DR EMBL; U92458; AB51765.1; -
 DR MIM; 604101; -
 DR GCRDB; GCR-1890; -
 DR GCRDB; GCR-2071; -
 DR PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.
 DR PFAM; PF01094; ANF_receptor; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KM Multigene family; Oligation; Polymorphism.
 KW SIGNAL
 FT CHAIN 1 32
 FT DOMAIN 33 915
 FT TRANSMEM 33 590
 FT TRANSMEM 591 615
 FT DOMAIN 616 627
 FT TRANSMEM 628 648
 FT TRANSMEM 649 654
 FT TRANSMEM 655 675
 FT TRANSMEM 676 702
 FT TRANSMEM 703 723
 FT TRANSMEM 724 753
 FT TRANSMEM 754 775
 FT TRANSMEM 776 788
 FT TRANSMEM 789 810
 FT TRANSMEM 811 825
 FT TRANSMEM 826 850
 FT TRANSMEM 851 915
 FT CARBOHYD 98 98
 FT CARBOHYD 458 458
 FT CARBOHYD 486 486
 FT CARBOHYD 572 572
 FT VARIANT 433 433
 SQ SEQUENCE 915 AA; 102250 MW; 1B278B39 CRC32;

Query Match 3.1%; Score 214; DB 1; Length 915;
 Best Local Similarity 22.9%; Pred. No. 6,48e-16;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

DB 597 LAMGII-ATIFVWATPIRYNDPIYASGRELSTVLTGIFLCY--IIF-L--MIA- 648
 QY 487 LTLIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLILGMLSTASIFLGLDGSFVSE 545
 DB 649 KPDVAVCSFRFVGLGMCISYALTLTKNRIYRIFEOGKRSVTAPRLISPTSLATSS 708
 QY 546 KTEFLICTRWILTVGTTAFGAMFAKTWRVHAIFKNYKMK-K-KIKDOKLVIYVG 602
 DB 709 LISVOLGVEI-WGVDPNIIID-YD-EHKTNPEQA-RGYLK-CDITDLOI-IGSL-G 761
 QY 603 MLTIDL-CILICWQAVDPLRTYRYSMEPDAGDISIRPLEHCENTHTATWLGIVYA 661
 DB 762 YSILIMV-TC-TVYAIKTRGVENENKAPIGFTMTTCIYWLAFIPFEGTAOSAKELY 819
 QY 662 YKGLMLFEGCLAMETRNVSIPA-LNDSKRYIGMSYVNGIMCIIGAAVSFLTRDOPWOF 720
 DB 820 IOTTLTISMLNSASVALGMLYMPKVIIFHELVNOKRKSF 863
 QY 721 C-IVALVI-I-FCSTITLCLVFPKLTITLTPNDATONRRROF 761
 RESULT 10
 ID MGR5_RAT STANDARD; PRT; 1203 AA.
 AC P31424;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
 GN GRM5 OR MGLURS.
 OS Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 92317054.
 RA ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;
 RT "Molecular characterization of a novel metabotropic glutamate
 RT receptor melurs coupled to inositol phosphate/Ca2+ signal
 RT transduction.";
 RT J. Biol. Chem. 267:13361-13368(1992).
 RN [2]
 RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-BRAIN;
 RX MEDLINE: 93343913.
 RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;
 RT "A variant of metabotropic glutamate receptor subtype 5: an
 RT evolutionally conserved insertion with no termination codon.";
 RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
 CC CHLORIDE CURRENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, 5A (SHOWN HERE) AND 5B, ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
 CC 32 RESIDUES.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
 CC CENTRAL NERVOUS SYSTEM.
 CC -1- MISCELLANEOUS: ACTIVATED BY OUTSOULATE > GLUTAMATE > IBOTENATE >
 CC TRANS-1- AMINOOCYCLOPENTYL-1,3-DICARBOXYLATE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST: TO MGLUR1.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: D10891; -; NOT ANNOTATED_CDS.
 DR EMBL: S64315; AAB27666.1; -;
 DR EMBL: A42916; A42916.
 DR GCRDB: GCR_0444; -;
 DR GCRDB: GCR_0760; -;
 DR PROSITE: PS00979; G-PROTEIN_RECP_F3_1; 1.
 DR PROSITE: PS00980; G-PROTEIN_RECP_F3_2; 1.
 DR PROSITE: PS00981; G-PROTEIN_RECP_F3_3; 1.
 DR PIR: PF00003; 7tm_3; 1.
 DR PIR: PF01094; ANF_receptor; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KM Multigene family; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 1 1203
 FT DOMAIN 22 578 METABOTROPIC GLUTAMATE RECEPTOR 5.
 FT TRANSMEM 579 601 I (POTENTIAL).
 FT DOMAIN 602 615 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 616 636 II (POTENTIAL).
 FT DOMAIN 637 647 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 648 666 III (POTENTIAL).
 FT DOMAIN 667 692 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 693 713 IV (POTENTIAL).
 FT DOMAIN 714 736 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 737 758 V (POTENTIAL).
 FT DOMAIN 759 771 VI (POTENTIAL).
 FT TRANSMEM 772 794 VII (POTENTIAL).
 FT DOMAIN 795 800
 FT TRANSMEM 801 826

FT DOMAIN 827 1203 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 86 88
 FT CARBOHYD 209 209 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 381 381 POTENTIAL.
 FT CARBOHYD 444 444 POTENTIAL.
 FT CARBOHYD 733 733 POTENTIAL.
 FT CARBOHYD 876 907 MISSING (IN ISOFORM 5A).
 SQ SEQUENCE 1203 AA; 131885 MW; 2955EA33 CRC32.
 Query Match 3.1%; Score 215; DB 1; Length 1203;
 Best Local Similarity 28.3%; Pred. No. 4,39e-16;
 Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;
 Db 655 AMYSALVTKRNIARILAGSK-KKCTKREMSACA-QLYAF-TILC---10-LGIT 707
 Oy 564 TTAAGAMFAKTRVHAIFKRWKMKKRIIKDKLIVYGGSLIDICILCMQAVDPLRRT 623
 Db 708 VALFMEPPDMDHDPSSIREYVLCNTNLGV-VTP-L-GYNGILL-L-SCTEFAKTRNVP 764
 Oy 624 VERSEMEPPAGRDI-SIRPLEHCENTHMTIWLGIYAVKGLMLFGC-FLAMETRNVS 681
 Db 765 -ANFNKATYAFMTTTCIIMLAFAVPY-YFGSNKTKITMCF-S-VSL-SATVALGCM-FV 818
 Oy 682 IPALNSKTIIGSVYNGVIGICIGAAVSFLTRDPNVQFCIALVIFGSIITL-CLVFFV 740
 Db 819 PKVYIIIAKPE 829
 Oy 741 PKLITLRTPD 751
 RESULT 11
 ID MGR5_HUMAN STANDARD; PRT; 1212 AA.
 AC PA1594;
 DT 01-NOV-1995 (rel. 32, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 15-DEC-1999 (rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
 GN GRM5 OR MGLURS.
 OS Homo sapiens (Human).
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 94197696.
 RA MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;
 RT "Molecular cloning and the functional expression of two isoforms of
 RT human metabotropic glutamate receptor subtype 5.";
 RL Biochem. Biophys. Res. Commun. 199:1136-1143(1994).
 RN [2]
 RP REVISIONS.
 RA KATSUKI F.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 860-952 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 93343913.
 RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;
 RT "A variant of metabotropic glutamate receptor subtype 5: an
 RT evolutionally conserved insertion with no termination codon.";
 RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
 CC CHLORIDE CURRENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, 5A (SHOWN HERE) AND 5B, ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
 CC 32 RESIDUES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST: TO MGLUR1.


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Db 681 AL-----IAKPTIGS-CVLOQRFQGVGFSIIYALLKTRNNISRIHFSASKSQRLKYPSP 735
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 537 GLDGESEFSEKFTFLCIVRTWILVGYTAFGAMFAKTRVHAIFENV-K-MKK-KIIND 593
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 736 OSOVVITSLIAIOVITIMMYEP-PGT--KEYY-PDR--REV-I---LK-CKTQDMS 784
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 594 QKLIIVGSLIDLCILICOWADPLRTVERYSMEPPAGHDISIRPLEHCENTHMT 653
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 FLFSOLYN-MILITICTIYAI-KTRKIP-ENENESKIGFTMYTTCIIMLAFAPYFGTG 841
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 654 IWLGIYAVYAGLMLFGCFLAMETRVNSIPALNDSKTIQMSYVNGIMCIGAAVSFLTR 713
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 842 NSEVQTTICISISLASVALVCL-YSPKVIYLVFHPD 879
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 714 DQPNVOFCIAVALIFECSTITL-CLVEFVPEKLITLRTNPD 751
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
ID CASR_RAT STANDARD: PRT; 1079 AA.
AC P48442;
AT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
DE CELL CALCIUM-SENSING RECEPTOR).
GN CASR OR PCAR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY OUTER MEDULLA;
RX MEDLINE; 95116508.
RA RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E.M., HERBERT S.C.;
RT "Cloning and functional expression of a rat kidney extracellular
RT calcium/polyvalent cation-sensing receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
RN [2]
RP SEQUENCE OF 1-294 FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE; 95241465.
RA RUAT M., SNOWMAN A.M., SNYDER S.H.;
RT "Calcium sensing receptor: molecular cloning in rat and localization
RT to nerve terminals.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
CC -1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U10354; AAC52149.1; -
DR EMBL; U20289; AAC52195.1; -
DR GCRDB; GCR1449; -
DR PROSITE; PS00979; G_PROTEIN_RECCEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECCEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECCEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein; signal.
FT SIGNAL 19 POTENTIAL.
FT CHAIN 20 1079 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
FT DOMAIN 20 612 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 613 635 I (POTENTIAL).
FT DOMAIN 638 649 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 650 670 II (POTENTIAL).
FT DOMAIN 671 681 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 682 700 III (POTENTIAL).
FT DOMAIN 701 724 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 725 745 IV (POTENTIAL).
FT DOMAIN 746 769 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 770 792 V (POTENTIAL).
FT DOMAIN 793 805 VI (POTENTIAL).
FT TRANSMEM 806 828 VI (POTENTIAL).
FT DOMAIN 829 836 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 837 862 VII (POTENTIAL).
FT DOMAIN 863 1079 VIII (POTENTIAL).
FT CARBOHYD 90 90 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 130 130 POTENTIAL.
FT CARBOHYD 261 261 POTENTIAL.
FT CARBOHYD 287 287 POTENTIAL.
FT CARBOHYD 386 386 POTENTIAL.
FT CARBOHYD 446 446 POTENTIAL.
FT CARBOHYD 468 468 POTENTIAL.
FT CARBOHYD 488 488 POTENTIAL.
FT CARBOHYD 541 541 POTENTIAL.
FT CARBOHYD 594 594 POTENTIAL.
SQ SEQUENCE 1079 AA; 120867 MW; 34118BE9 CRC32;

Query Match 2.94; Score 199; DB 1; Length 1079;
Best Local Similarity 29.78; Pred. No. 2,04e-13;
Matches 27; Conservative 30; Mismatches 34; Indels 0; Gaps 0;

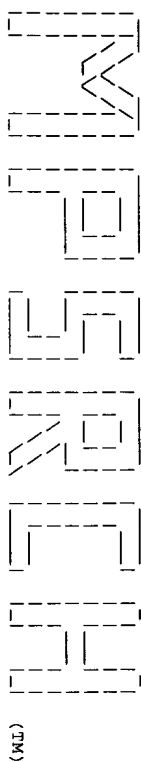
Db 125 LDFECNCEHPISTIAVCGATGSGVSTAVANLLGLEPIQVSVASSRSLSKNKKKSL 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 113 LKAFYDAIKKGRHNLAVFGVCSVSTIASELSQGNVLVLSFAATTPVLADKKKPYPF 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 RTIPNDEHQTAMADIIETFRMNVGTIAD 215
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 173 RTVPSDNAVNPALIKLKHFRMRVGTITPD 203
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
ID MGR2_HUMAN STANDARD: PRT; 872 AA.
AC Q14416;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GN GRM2 OR MGUR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95346007.
RA FLOR P.J., LINDAUER K., PUTTNER I., RUEGG D., LUKIC S., KNOFFEL T.,
RA KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 2.";
RL Eur. J. Neurosci. 7:622-629(1995).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC MAY MEDATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE
CC ADULT BRAIN AS WELL AS IN FETAL BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGUR3.
CC -----
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ID	FASTA	STANDARD	PRT	1078 AA
AC	PA1180: Q13912: Q16379; Q16108: Q16109; Q16110:			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).			
DE	CASR OR PCAR.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.			
OC	[1]			
RN	SEQUENCE FROM N.A.			

RA PEARCE S.H.S., THAKKER R.V.:
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN
RP
RC TISSUE-PARATHYROID;
RX MEDLINE; 95279439.
RA GARRITT J.E., CAUVANO I.V., HAMMERLAND L.G., HUNG B.C., BROWN E.M.,
RA HERBERT S.C., NEMETH E.F., FULLER F.;
RT "Molecular cloning and functional expression of human parathyroid
RT calcium receptor cDNAs.";
RL J Biol. Chem. 270:12919-12925(1995).
RN
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE; 95408281.
RA AIDA K., KOISHI S., TAMATA M., ONAYA T.;
RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
RL human kidney";
RN Biochem. Biophys. Res. Commun. 214:524-529(1995).
RN
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96343808.
RA FEIGHEL M., ZINK-LORENZ A., HOLLOSCHI A., HAFNER M., FLOCKERZI V.,
RA RADE F.;
RT "Expression of a calcium-sensing receptor in a human medullary
RT thyroid carcinoma cell line and its contribution to calcitonin
RT secretion";
RL Endocrinology 137:3842-3848(1996).
RN
RN [5]
RP VARIANTS FHh GLU-185, LYS-297 AND TRP-795,
RX MEDLINE; 94094324.
RA POLLAK M.R., BROWN E.M., CHOU Y.H., HERBERT S.C., MARX S.J.,
RA STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G.;
RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
RT hypocalcaemic hypercalcaemia and neonatal severe
RT hyperparathyroidism";
RL Cell 75:1297-1303(1993).
RN
RN [6]
RP VARIANT ADH ALA-127.
RX MEDLINE; 95179179.
RA POLLAK M.R., BROWN E.M., ESTEP H.L., MCCLAIN P.N., KIFOR O., PARK J.,
RA HERBERT S.C., SEIDMAN C.E., SEIDMAN J.G.;
RT "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor
RT gene mutation.";
RL Nat. Genet. 8:303-307(1994).
RN
RN [7]
RP VARIANTS FHh MET-62, CYS-66; MET-138; GLU-143 AND GLN-227,
RX MEDLINE; 95243222.
RA CHOU Y.-H.W., POLLAK M.R., BRANDI M.L., TOSS G., ARNOVIST H.,
RA ATKINSON A.B., PAPADOPOULOS S.E., MARX S., BROWN E.M., SEIDMAN J.G.,
RA SEIDMAN C.E.;
RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
RT familial hypocalcaemic hypercalcaemia";
RL Am. J. Hum. Genet. 56:1073-1079(1995).
RN
RN [8]
RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHh ALA-39.
RX MEDLINE; 95403641.
RA AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAMATA M., ONAYA T.;
RT "Familial hypocalcaemic hypercalcaemia associated with mutation in the
RT human Ca(2+)-sensing receptor gene";
RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
RN
RN [9]
RP VARIANTS NSHPT LEU-227 AND TYR-598.
RX MEDLINE; 96292293.
RA PEARCE S.H.S., TRUMP D., WOODING C., BESSER G.M., CHEW S.L.,
RA GRANT D.B., HEATH D.A., HUGHES I.A., PATTERSON C.R., WHYTE M.P.,
RA THAKKER R.V.;
RT "Calcium-sensing receptor mutations in familial benign hypercalcaemia
RT and neonatal hyperparathyroidism";
RL J. Clin. Invest. 96:2683-2692(1995).
RN
RN [10]
RP VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851,
RX MEDLINE; 96311554.



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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Mar 15 21:55:28 2000; MasPar time 64.25 seconds
690.163 Million cell updates/sec
Tabular output not generated.

Title: >US-09-211-755-4
Description: (1-940) from US09211755.pep
Perfect Score: 6906
Sequence: 1 MASPPSSGQPRPPPPPPPPA.....TASPRHRHVPSPFRWVWSGL 940

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir62
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 55.689; Variance 124.230; scale 0.448

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1658	24.0	960	2 JE0356	gamma-aminobutyric ac	2.79e-273
2	1240	3.5	908	2 I49142	metabotropic glutamat	3.04e-17
3	236	3.4	871	2 A46742	metabotropic glutamat	1.23e-16
4	225	3.3	912	2 I58149	metabotropic glutamat	5.49e-15
5	225	3.3	912	2 JH0563	metabotropic glutamat	5.49e-15
6	214	3.1	915	2 A49874	metabotropic glutamat	2.32e-13
7	216	3.1	940	2 T02740	hypothetical protein	1.18e-13
8	215	3.1	1171	2 A42916	metabotropic glutamat	1.66e-13
9	215	3.1	1180	2 J02132	metabotropic glutamat	1.66e-13
10	215	3.1	1212	2 UC2131	metabotropic glutamat	1.66e-13
11	197	2.9	1078	2 S49341	calcium-sensing recep	6.71e-11
12	199	2.9	1079	2 I59362	calcium/polyvalent ca	3.47e-11
13	190	2.8	898	2 T05099	hypothetical protein	6.58e-10
14	194	2.8	1078	2 A56715	calcium receptor (clo	1.79e-10
15	192	2.8	1085	2 S40476	Ca(2+)-sensing recept	3.44e-10
16	194	2.8	1088	2 B56715	calcium receptor (clo	1.79e-10
17	186	2.7	872	2 JH0561	metabotropic glutamat	2.40e-09
18	188	2.7	879	2 JH0562	metabotropic glutamat	1.26e-09
19	178	2.6	1199	2 A41939	G protein-coupled glu	3.07e-08
20	180	2.6	1218	2 S71376	glutamate receptor ho	1.63e-08
21	164	2.4	986	1 OYURGA	speract receptor prec	2.37e-06
22	165	2.4	1108	2 B55915	guanylate cyclase (EC	1.75e-06
23	154	2.2	1525	1 A56699	guanylate cyclase (EC	4.79e-05

24	148	2.1	373	2 A36125	branched-chain amino	2.78e-04
25	144	2.1	938	2 T01809	hypothetical protein	8.78e-04
26	146	2.1	958	2 T02741	hypothetical protein	4.95e-04
27	142	2.1	1005	2 S33525	guanylate cyclase (EC	1.55e-03
28	145	2.1	1125	1 OYURCP	speract receptor prec	6.60e-04
29	136	2.0	1679	2 T15968	hypothetical protein	8.33e-03
30	134	1.9	430	2 B69955	conserved hypothetical	1.44e-02
31	132	1.9	535	2 A54155	natriuretic peptide r	2.45e-02
32	130	1.9	536	2 S71332	natriuretic peptide c	4.28e-02
33	129	1.9	536	2 A45409	atrial natriuretic pe	5.59e-02
34	129	1.9	537	1 A28111	natriuretic peptide r	5.59e-02
35	128	1.9	637	2 C65129	hypothetical ABC tran	7.30e-02
36	130	1.9	1103	2 UC5581	guanylate cyclase (EC	4.28e-02
37	132	1.9	1108	2 I59385	guanylate cyclase (EC	2.49e-02
38	124	1.8	358	2 B69826	hypothetical protein	2.09e-01
39	125	1.8	404	1 LABECA	latent membrane prote	1.61e-01
40	126	1.8	540	1 OYURCR	natriuretic peptide r	1.24e-01
41	125	1.8	662	2 D40228	neurexin II-beta prec	1.61e-01
42	124	1.8	676	2 OYUR084	myosin heavy chain, f	2.09e-01
43	126	1.8	1047	1 OYRTBR	atrial natriuretic pe	2.09e-01
44	124	1.8	1065	2 G72330	hypothetical protein	2.09e-01
45	123	1.8	1937	2 I38055	myosin heavy chain, p	2.72e-01

ALIGNMENTS

RESULT	1	JE0356	#type complete
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TITLE	GABA(B) receptor		
ALTERNATE_NAMES	#formal_name Homo sapiens #common_name man		
ORGANISM	05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change		
DATE	12-Feb-1999		

ACCESSIONS	JE0356
REFERENCE	Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante, L.; Gasparini, P. Biochem. Biophys. Res. Commun. (1998) 250:240-245
#journal	GABA (gamma-aminobutyric acid) neurotransmission: Identification and fine mapping of the human GABAB receptor gene.
#title	

#cross-references	MUID:98440782
#accession	JE0356
#molecule_type	mRNA
#residues	1-960 #label GRI
#cross-references	GB:Y11044; NID:q2826760
##note	this ORF is not annotated in Genbank entry HSGTHA1, release 109

GENETICS

#map_position	6p21.3-6p21.3
KEYWORDS	glycoprotein; neurotransmitter receptor; transmembrane protein

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1-11	#domain signal sequence #status predicted #label SIG\
1-960	#product gamma-aminobutyric acid receptor B #status predicted #label MAT\
590-613	#domain transmembrane #status predicted #label TM1\
629-654	#domain transmembrane #status predicted #label TM2\
666-687	#domain transmembrane #status predicted #label TM3\
709-730	#domain transmembrane #status predicted #label TM4\
767-788	#domain transmembrane #status predicted #label TM5\
803-825	#domain transmembrane #status predicted #label TM6\
831-856	#domain transmembrane #status predicted #label TM7\
23,83,439,481,501,513,630	#binding site carbohydrate (Asn) (covalent) #status predicted

SUMMARY	#length 960 #molecular_weight 108148 #checksum 3766
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Matches	248; Conservative 177; Mismatches 247; Indels 16; Gaps 14;

DB	184 GQACQAVENALEDVNSRDILPDYELKLIHDSKCDPOQAKYLYELLYNDPIIILMP 243
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QY 73 GRGVLPVEALAIQIRNE-SLRRPYFLDLRLDYDECDNAAGLKAFAFYDAIKYGNHLMVWG 131
Db 244 G-CSSVSTVIAEAARMNLLVLSYSSPALSNRORPPEFRHPATILNPRVLEFK 302
QY 132 GVCPSVSTIAESIQGNLVLSFAATTPVLAKKKYPFFRVPDANVPKLTLLH 191
Db 303 GKKKATLTIQOTTEVTSTLDLEERKENGIEITFRQSFSDPAVPKLRKODARITV 362
QY 192 FRRRRVGTTLQDQRFSEVENDLTGLVLYGEDIISDTESNDPCISVKKLGNDRITL 251
Db 363 GLYEYFARVCEYKERLFKKYWFLLGWADWVF-KIY-DP-SINCYDENTEAIVE 419
QY 252 GQPDQNNAAVFCFAEFSEFSGKYQWILPGWEPAWMDQVHEANSSCLRRSLIAAME 311
Db 420 GHITTEIVMLNPANTRISNMTSQEFVEKLRKLRHPERTGGFOAPALAIAMALAA 479
QY 312 GIYGVPEPLSSKOITISKTPQY-EREYNS-KRSGVPSKFH-G-YAIDGIMYIAKT 367
Db 480 LAKTSGG--GGRSGVRLEDFNNQTTDQIYRANSSSEFEGVSGHVVDASGSRMAWTL 537
QY 368 LQAMETLHASRHRIODFNYTDHLGKILINAMNETNFEVGTGVVF-RNGERMGTIK 426
Db 538 IEPOGGSYKIGIYDSTDDLSM-SKTDKMGSGPPADQTVITFRFLSQKFLISYV 596
QY 427 FTQPDQREKVEYNAVADTEITINDTIRFOGSEPPKDKTITLQLRKISDPLYSLSA 486
Db 597 LSSGLIVAVCLSFNIYSHVAYIONOPNLNLTAAGCSALAAVPLGLDGHYIGN 656
QY 487 LTLGIMASAFLEFNKRNOKLIKMSPPYNNLLILGMLSYASIFLFGDGSFVSK 546
Db 657 QPFVQQAALMLIGLFGSLGYSMTKIMWHITGFKKEKEMKLTLEPWLATVGLL 716
QY 547 TFFTLCTVFWTLTVGYTTAFGMAFKATWRHAIF--KKNVKK-KKIIDQCLIVYGM 603
Db 717 VGMADVLTIAWQVDPDLHRTIEFAKEEPKEDIVSILPOLHSGSRKNNWLGIFYCYK 776
QY 604 LILDLICILCMQAVDPLRRTVERYSMEPPAGRDISTIRPLEHCETHHTWLGIVAYK 663
Db 777 GLLILGILVAVETKSVSTERINDHRAVMAIYNAVLCLITAPYTMILSSQDAAFAFA 836
QY 664 GLMLFEGCFIAMEYRNVSPALNDSKYIGMSYVNGIMCIICAANSFLRQDPNVQFIV 723
Db 837 SLAIVSSYITLVLPVKRRLIRGE 864
QY 724 ALVILFCSTTLCLVFPKRLITLRINPD 751

RESULT 2
ENTRY 149142 #type complete
TITLE metabotropic glutamate receptor 8 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
ACCESSIONS 149142
#authors Duvoisin, R.M.; Zhang, C.; Ramonell, K.
#journal J. Neurosci. (1995) 15:3075-3083
#title A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.
#cross-references MUID:95239344
#accession 149142
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-908 ##label RES
#cross-references EMBL:U17252; NID:g854728; PIDN:AAA6149.1;
PDB:g854729

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#gene mGluR8
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS neurotransmitter receptor
SUMMARY #length 908 #molecular-weight 101413 #checksum 2996
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Db 584 AAVPVLAILGII-ATFEVITFEVRYNDPTVRASGRELSSVLLTGLFYCYSTIFLM-I- 640
QY 482 SILSAL-TILGIMASAFLEFN-IKNNQKLIKMSPPYNNLLILGMLSYASIFLFGD 539
Db 641 AA--PD-TI--ICGFRIELFGKCSYALLLTKTNRIHRIEFGKKSVTAPKFSPASQ 695
QY 540 GSEVSEKTFETLCTVRWTLTVGYTTAFGMAFKATWRHAIFKNVKK-K-KIIDOKL 596
Db 696 LVTFSLISVOLGCVFVFWVDPPHTIID-YG-EQRTIDPE-NARGVYK-CDISDLSL-I 750
QY 597 LVYGMMLLDCLICMCAVDPDLRRTVERYSMEPPAGRDISTIRPLEHCETHHTWIL 656
Db 751 CSL-GYSILMV-TC-TVYAIKTRGVPEFNEAKPIGFTWYTCIILMAPIPFQTAOS 807
QY 657 GIYVAYKGLMLFEGCFIAMEYRNVSP-ALNDSKYIGMSYVNGIMCIICAANSFLTRDQ 715
Db 808 AEKMYIOTTLTVMSLSASVSGMLMPKVYIITHPEQNOVKRRKSF 856
QY 716 PNVQFC-IVALVI-I-FCSTTLCLVFPKRLITLRINPDAAQONRRFQF 761

RESULT 3
ENTRY A46742 #type complete
TITLE metabotropic glutamate receptor, mGluR6 - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
ACCESSIONS A46742
#authors Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
#journal J. Biol. Chem. (1993) 268:11868-11873
#title Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6 with a high agonist selectivity for L-2-amino-4-phosphonobutylate.
#cross-references MUID:93280152
#accession A46742
#status preliminary
#molecule_type nucleic acid
#residues 1-871 ##label NAK
#cross-references GB:D13963; NID:g391856; PIDN:BA03066.1;
PID:d1003572; PID:g391857
#experimental_source retina
#note sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P133250)
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 871 #molecular-weight 95088 #checksum 3942

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Best Local Similarity 22.9%; Pred. No. 1,23e-16;
Matches 64; Conservative 90; Mismatches 102; Indels 24; Gaps 21;

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QY 487 LTLGIMASAFLEFNKRNOK-LIKMSPPYNNLLILGMLSYASIFLFGDGSFVSE 545
Db 639 PC-AICAARLLILGTTLSYALLTKTNRIYRIFEDGKRSVPPRISPSQSLVITFG 697
QY 546 KTFEELCTVFRWTLTVGYTTAFGMAFKATWRHAIFKNVKK--MKKK-IKKOKLLVYGG 602
Db 698 LLSLVGVGYIANLGAQPPSYVD-YE-EQRTVDPQA-RGVYK-CDMSDLSL-IGCL-GY 751
QY 603 MLTIDICILCMQAVDPLRRTVERYSMEPPAGRDISTIRPLEHCETHHTWILGIYAY 662
Db 752 -SLLMWTC-TVYAIKARGVPEFNEAKPIGFTWYTCIILMAPIPFQTAQSAEKIYI 809
QY 663 KGLMLFEGCFIAMEYRNVSP-ALNDSKYIGMSYVNGIMCIICAANSFLTRDQPNVQFC 721
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#title	Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid-sensitive class of metabotropic glutamate receptors.	
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#accession	I57954	
#status	preliminary; translated from GB/EMBL/DBJ	
#molecule_type	mRNA	
##residues	1-915	#label RE2
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Best Local Similarity	22.9%; Pred. No.2,32e-13;	
Matches	65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;	
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Qy	487 LTILGMASAFLEFN-IKNRNOKLIKMSPPYNNNIIILGMLSYASIFLFGIDSEFVSE 545	
Db	649 KPDVASFRRVFVGLDMCISYALLKTRIRYIFEDGKKSTVAPRLSPSOLATISS 708	
Qy	546 KTFETLCVRWILTVGGTTFAGFMFKTRVVAIRRWKKM-K-KITKDKKLVIYVG 602	
Db	709 LISVOLLGVFI-WGVDPPIIID-D-EKRTNPEQA-RGVLR-CDITDLOI-ICSL-G 761	
Qy	603 MLLIDL-CILICQWADVPLRRTVERSMEDDPAGRIDISIRPLEHENHMTIWIYIA 661	
Db	762 YSLILAV-TC-TVAATRGVPERNFENAKIGCTWTTCIWLALPIFFGASHEKLY 819	
Qy	662 YKGLIMEFGELAEIRNVSIPA-LNDSKIKGMSYVNVGIMCIGAASFEIIRDPNQVF 720	
Db	820 IQTTLTISNMLASVALGMLVPKYIIIFHELMVOKRKRSF 863	
Qy	721 C-IVALVI-I-FCSTITLCIVFVPKLITLTNPDAATONRRPOF 761	
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TITLE	hypothetical protein T914.18 - Arabidopsis thaliana	
ORGANISM	#formal_name Arabidopsis thaliana #common_name mouse-ear cress	
DATE	24-Mar-1999	#sequence-revision 24-Mar-1999 #text_change 23-Apr-1999
ACCESSIONS	T02740	
REFERENCE	T14710	
#authors	Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Romling, C.M.; Fraser, C.M.; Somerville, C.R.; Venter, J.C.	
#submission	Submitted to the EMBL Data Library, August 1998	
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OY	153	LSFATIPVLADKKKKYFEFTVPSDVAAPVALLKLKLFHFRMRVGLTQDVQREFSSVFN	212
Db	180	PFPLDALODVYKRSVIPPEAIDIEICKELKLMERQARVYVHMESSLARVFOIARDI	239
OY	213	D-LTGLVGLDIE--ISDTSEFSNDPCTSVKIKUKGNDVRIILIGOFQDNMAAKVFCACFEE	269
Db	240	GMMEGYVWLM	250
OY	270	SMFGSKTOWII	280
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DATE	04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999		
ACCESSIONS	A42916		
REFERENCE	A42916		
authors	Abe,T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.		
#journal	J. Biol. Chem. (1992) 267:13361-13368		
#title	Molecular characterization of a novel metabotropic glutamate receptor mglur5 coupled to inositol phosphate/cas2+ signal transduction.		
#cross-references	MUTID:92317054		
#accession	A42916		
#molecule	preliminary		
#status	preliminary		
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#experimental_source	brain		
#note	sequence extracted from NCBI backbone (NCBIN:107749, NCBIPI:107750)		
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OY	564	TTATGAMFAKWRHAHAFKNVKKKKIKIIOQKLLIVYGMLLIDLCILCQWADPLRRT	623
Db	708	VALFMEPPDIDMHDPISIREYLLICNTNTNGV-VTPP-LGYNGLLIT-SCFYAFKTRNP	764
OY	624	VERSMEDPDAGRII-SIRPLEHCENTHTMTIMGLIYAAKGLMLPFC-FLAMETRRNS	661
Db	765	-ANFNKAQYIAFYTCITIMLAFVPI-YFGSNKIKITMCF-S-VSL-SATVALGCM-FV	818
OY	682	IPALNDSKYSIYSYNYGIMCIIGAAVSFLTRDPQNVQFCIVALVILIFCSTIL-CLAFV	740
Db	819	PKYVILIAKPE	829
OY	741	PKLITLRTNP	751
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TITLE	metabotropic glutamate receptor 5 A - human		
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DATE	28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996		
ACCESSIONS	JC2132		
REFERENCE	JC2131		
authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994) 199:1136-1143		
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
#cross-references	MUTID:94197696		

QY 640 IPALNDSKIVGSMVYVNGIMCIIGAAVSFLRDQPNVQFCIVAVIIFCSTTL-CLVEFV 698
DB 820 PVIYIILAKPE 830
| : : : : :
QY 699 PKLITLRTNPD 709

RESULT 13
ID US-08-072-574-12 STANDARD: PRT: 877 AA.
AC xxxxxx
XX
XX
XX

Sequence 12, Application US/08072574

Sequence 12, Application US/08072574
Patent No. 5521297
GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen
APPLICANT: Pontsler, Aaron
TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 00719

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,574
FILING DATE: 19930604
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
TELEFAX: 213-489-4210
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 877 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 877 AA; 98138 MW; 4163481 CN;

Query Match 2.8%; Score 181; DB 1; Length 877;
Best Local Similarity 26.2%; Pred. No. 2,35e-04;
Matches 50; Conservative 58; Mismatches 64; Indels 19; Gaps 17;

DB 656 AMSSALVTKNRIARILASGK-KKICPKRPMASQA-OLVAF-ILIC---IO-LGIT 708
| : : : : :
QY 522 TTAGGAFKATWRAHAFKYNKMKKIIKDKLIVIGMMLDLCILICWQAVDPLRT 581
DB 709 VALFIMEPPDLMHDYPSIREVYLICNTNLGV-VTPL-GNNGLLIL-SCFFYAEKTRNPV 765
| : : : : :
QY 582 VEKYSMEDPAGRDI-SIRPLEHCENTHMTIWIGIVATKGLMLDFGC-FLAMETRNVS 639
DB 766 -ANPEAKYALIMTYTCIKWIAFVPI-YFGSNYKIITMGF-S-VSL-SATVALGCM-EV 819
| : : : : :
QY 640 IPALNDSKIVGSMVYVNGIMCIIGAAVSFLRDQPNVQFCIVAVIIFCSTTL-CLVEFV 698

DB 820 PVIYIILAKPE 830
| : : : : :
QY 699 PKLITLRTNPD 709

RESULT 14
ID US-08-072-574-6 STANDARD: PRT: 879 AA.
AC xxxxxx
XX
XX
XX
XX

Sequence 6, Application US/08072574

Sequence 6, Application US/08072574
Patent No. 5521297
GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen
APPLICANT: Pontsler, Aaron
TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 00719

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,574
FILING DATE: 19930604
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
TELEFAX: 213-489-4210
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 879 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 879 AA; 98878 MW; 4241110 CN;

Query Match 2.8%; Score 187; DB 1; Length 879;
Best Local Similarity 34.6%; Pred. No. 8,85e-05;
Matches 28; Conservative 26; Mismatches 26; Indels 1; Gaps 1;

DB 145 VIGGSYSVSIQVANLLFQIPQISVASTSAKLSRXYDFARTVPPDFYQAKAAEI 204
| : : : : :
QY 87 VEGVCPSTVSTIASELSLOGWMLVOLSFATTPVLADKKRYPFPRTVSDNAVNPATIKL 146
DB 205 LRFENMTVSTVYASQCD-XGE 224
QY 147 LKHVQMKRKGITLDVQRFSE 167

RESULT 15
ID US-08-486-270-6 STANDARD: PRT: 879 AA.
AC xxxxxx
XX

DT Sequence 6, Application US/08486270
 XX
 DE
 CC Sequence 6, Application US/08486270
 CC Patent No. 5807889
 CC GENERAL INFORMATION:
 CC APPLICANT: Daggett, Lorrie
 CC APPLICANT: Ellis, Steven B.
 CC APPLICANT: Liaw, Chen
 CC APPLICANT: Pontsler, Aaron
 CC APPLICANT: Johnson, Edwin C.
 CC APPLICANT: Hess, Stephen D.
 CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
 CC TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
 CC NUMBER OF SEQUENCES: 13
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 CC STREET: 444 South Flower Street, Suite 2000
 CC CITY: Los Angeles
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 90071
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/486,270
 CC FILING DATE: 02-JUN-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/072,574
 CC FILING DATE: 04-JUN-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Reiter, Stephen E.
 CC REGISTRATION NUMBER: 31,192
 CC REFERENCE/DOCKET NUMBER: FP41 9772
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-546-4737
 CC TELEFAX: 619-546-9392
 CC INFORMATION FOR SEQ ID NO: 6:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 879 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 879 AA; 98878 MW; 4241110 CN;
 SQ
 Query Match 2.8%; Score 187; DB 1; Length 879;
 Best Local Similarity 34.6%; Pred. No. 8.85e-05;
 Matches 28; Conservative 26; Mismatches 26; Indels 1; Gaps 1;
 Db 145 VIGSGYSVSIIQVANLRLFIQIPISTASTSAKLSRDIYFARTVPPDFYQAKMAEI 204
 Oy 87 VEGVCPEVTSIIAESIQGMNLVQLSEFATPTVLADKKKYPFFRTVPSDNVAVNPAILKL 146
 Db 205 LRFEMTIVSTVABGD-YGE 224
 Oy 147 LKHYQWKRVGTLTDVQRFSE 167

Search completed: Wed Mar 15 21:45:33 2000
 Job time : 34 secs.

QY 150 YQMRVGTLLQDVQRFSEVRNDLTGLVYGEDIETSDTESFSNDPCTSVKRLKNDVRIIL 209
Db 196 GLFETEARKEVCEVYKERLFSGKKYWFLLIGWYADNMF-KIY-DP-SINCTVDEMTAVE 252
QY 210 GQFQNNAAKVFCCAYEENMGSKYQWIIIPGWYEPSMEQVHTAANSRCLRKMLLAAME 269
Db 253 GHITTEIVMLNPANTRSISNMTSOEFVEKLTFRKRPDETGFOEAPLAYDAIMALALA 312
QY 270 GYGVDEPLSSQKIKTISGKTPOQY-EREYNN-KRSGVPSKFH-G-YAIDGIWVIAKT 325
Db 313 LNKISGG--GGRSGVRLEDEFNNOITDQIYRAMNSSSFGVSGHYVFDASGRMAATL 370
QY 326 LQRMETLHASSRHQRIDQFNTHDILGRILLNMANETNEFGVIGQVVF-RNGERMGITK 384
Db 371 IEQLOGSGYKRIGYDSTKQDLMSW-SKTDKWIQSGPPADQTLVKTFRLSQKLFISVS 429
QY 385 FTQQRDSREKVGVEYNVADTLEIINDTIRQSGSEPRDKTIIIEQLRKISLPLXSILSA 444
Db 430 LSSIGIYLAVVCISFNINSHVRYIONSQPNLNLTAVGCSLAAVFPGLDGYHIGRN 489
QY 445 LTIIGMIMASAFLEFNNKRNQKLIKMSPPYNNLIILGMLSYASIFLFGDGSFVSEK 504
Db 490 QPFPVQCARLMLLGLGSLGSGMFTKIWWHTVFTKKEKEMRKLTLEPKKIATVGL 549
QY 505 TFEFLCTVRFWILTVGYTFAFGAMFAKTWRVHALF--KNVKKM-KKIKQKLLVIYGM 561
Db 550 VGMQVTLTAIQVDPHRTIETFAKEPEKEDIVSILPOLEHSSRKMTWLGIFYGK 609
QY 562 LITDCLILICQAVDPLRKRYEKSMEPDAGRDISIRPLEHECENHMTIMLVIYAYK 621
Db 610 GLLLIGIFLAYETKSVSTEKINDHRAVGMAIYNVAVLICITAPVIMLLSQODAAFAFA 669
QY 622 GLIMLFCFLAMETRVNSIPALNDSKYIGMSYVNGVICITGAIVSFLTRDQPNVQCIY 681
Db 670 SLAIVSSYITLVVLFVPKMRRLITRGE 697
QY 682 ALVITFCSTITLCLVFPVKLITRTNPD 709

RESULT 2
ID W40119 standard; Protein: 844 AA.
AC W40119;
DT 03-JUN-1998 (first entry)
DE Human GABA-BR1b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1a/B receptor; human; brain; agonist;
inhibitory neurotransmitter; peripheral nervous system; antagonist;
treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
epilepsy; cognitive function.
OS Homo sapiens.
PN MO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR N-PSDB: V10267.
PT Purified GABA-B receptor or receptor protein - and antagonists of
these which may be useful in treating nervous system disorders
PS Claim 4: Page 86-90; 108pp; English.
CC This sequence represents a novel human GABA-B receptor protein,
GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 844 AA;

Query Match 25.7%; Score 1687; DB 1; Length 844;

Best Local Similarity 36.2%; Pred. No. 1,04e-131;
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;
Db 68 GQACQPAVENALDEVDNSRDILDPYELKLIHNSKCDPGCATYLYVELLYNDPIKTIILMP 127
QY 31 GRGLPAVEALIDQIRNE-SILRPYFLDLRLYDTECNAGKAFYDAIKYGRPHHLAVFG 89
Db 128 G-CSSVSTLVAEAAKMNLLIVLSGSSSPALSNRQRPPEFRHPSTLNPVRVTKFEK 186
QY 90 GVCPSVTSTIAESLQGNLVQLSFAATTPVADKCKIPTYFRVPSDNAAVNPALKLKH 149
Db 187 WGMKRIATIQOTTEVFSTLDDLEERYKEAGIEITFRQSFSPDPAVYKMLKQDAIIV 246
QY 150 YQMRVGTLLQDVQRFSEVRNDLTGLVYGEDIETSDTESFSNDPCTSVKRLKNDVRIIL 209
Db 247 GLFETEARKEVCEVYKERLFSGKKYWFLLIGWYADNMF-KIY-DP-SINCTVDEMTAVE 303
QY 210 GQFQNNAAKVFCCAYEENMGSKYQWIIIPGWYEPSMEQVHTAANSRCLRKMLLAAME 269
Db 304 GHITTEIVMLNPANTRSISNMTSOEFVEKLTFRKRPDETGFOEAPLAYDAIMALALA 363
QY 270 GYGVDEPLSSQKIKTISGKTPOQY-EREYNN-KRSGVPSKFH-G-YAIDGIWVIAKT 325
Db 364 LNKISGG--GGRSGVRLEDEFNNOITDQIYRAMNSSSFGVSGHYVFDASGRMAATL 421
QY 326 LQRMETLHASSRHQRIDQFNTHDILGRILLNMANETNEFGVIGQVVF-RNGERMGITK 384
Db 422 IEQLOGSGYKRIGYDSTKQDLMSW-SKTDKWIQSGPPADQTLVKTFRLSQKLFISVS 480
QY 385 FTQQRDSREKVGVEYNVADTLEIINDTIRQSGSEPRDKTIIIEQLRKISLPLXSILSA 444
Db 481 LSSIGIYLAVVCISFNINSHVRYIONSQPNLNLTAVGCSLAAVFPGLDGYHIGRN 540
QY 445 LTIIGMIMASAFLEFNNKRNQKLIKMSPPYNNLIILGMLSYASIFLFGDGSFVSEK 504
Db 541 QPFPVQCARLMLLGLGSLGSGMFTKIWWHTVFTKKEKEMRKLTLEPKKIATVGL 600
QY 505 TFEFLCTVRFWILTVGYTFAFGAMFAKTWRVHALF--KNVKKM-KKIKQKLLVIYGM 561
Db 601 VGMQVTLTAIQVDPHRTIETFAKEPEKEDIVSILPOLEHSSRKMTWLGIFYGK 660
QY 562 LITDCLILICQAVDPLRKRYEKSMEPDAGRDISIRPLEHECENHMTIMLVIYAYK 621
Db 661 GLLLIGIFLAYETKSVSTEKINDHRAVGMAIYNVAVLICITAPVIMLLSQODAAFAFA 720
QY 622 GLIMLFCFLAMETRVNSIPALNDSKYIGMSYVNGVICITGAIVSFLTRDQPNVQCIY 681
Db 721 SLAIVSSYITLVVLFVPKMRRLITRGE 748
QY 682 ALVITFCSTITLCLVFPVKLITRTNPD 709

RESULT 3
ID W40118 standard; Protein: 844 AA.
AC W40118;
DT 03-JUN-1998 (first entry)
DE Rat GABA-BR1b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;
inhibitory neurotransmitter; peripheral nervous system; antagonist;
treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
epilepsy; cognitive function.
OS Rattus norvegicus.
PN MO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR N-PSDB: V10266.
PT Purified GABA-B receptor or receptor protein - and antagonists of
these which may be useful in treating nervous system disorders


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OY 498 GSFSEKFFETLCYVFWMLVGGYTAFGAMFAKTRVHAIFKNVK--MKK-KIINDOKL 554
DB 700 LAIFSLISLOL-LGICWVWVDPSHVD-FODORTLDR-PA-GRVLK-CDMSDLSL- 753
OY 555 LVIYVGMILDLCLIC-WQAVDPLRTRVEKYSMEPPPARDRDISIRPLEHCNTHMTWT 613
DB 754 ICLL-GYMLLMV-TC-TVYAIKRGVPEPTEAKPIGFTWYTCIWLAFIPDFGTSQ 810
OY 614 LGIYVAYKGLMLFGCFLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIIGAIVSLTRD 672
DB 811 SADKLYIOTTLTVSVLSASVSLGMLYMPKVYIILFPEONPKRK 857
OY 673 QPNVQFC-IVALVT-I-FCSTITLCIVFVPRKLITLRNPDAATQNR 716

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RESULT 10
ID W01099 standard; Protein: 877 AA.
AC W01099;
DR 03-JAN-1997 (first entry)
DE Metabotropic glutamate receptor subtype mglur6.
KM Metabotropic glutamate receptor; mglur6; neurological disease;
KW neurotransmitter.
OS Homo sapiens.
PN W09629404-A1.
PD 26-SEP-1996.
PF 18-MAR-1995; U03662.
PR 20-MAR-1995; US-407875.
PA (SIBIR) SIBIA NEUROSCIENCES INC.
PI Daggett LP, Lu C;
DR WPI; 96-443180/44.
DR N-PSDB; T38322.
PT Human metabotropic glutamate receptor and related nucleic acid -
PT useful to identify related receptor subtypes and e.g. for drug
PT screening
PS Claim 2; Page 66-68; 79pp; English.
CC Novel human metabotropic glutamate receptor protein subtype mglur6
CC (W01099) participates in the G-protein-coupled response of cells to
CC glutamatergic ligands. Its amino acid sequence was determined from
CC cDNA clones (see also T38322) ctd. from a human retinal cDNA library.
CC A splice variant has an alternative N-terminal sequence (see also
CC W01100). Recombinant receptors, practically free of contamination
CC by other receptors, can be produced in host cells. The receptors,
CC and cells expressing them, are used in drug screening to identify
CC cpts. that modulate mglur6.
SQ Sequence 877 AA;

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Query Match 3.4%; Score 225; DB 1; Length 877;
 Best Local Similarity 21.5%; Pred. No. 1.84e-07;
 Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

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DB 592 LAVIGIVTTTVAATFVRYNNTPIYRASGRSLVLLTGIFLYA-I-YF-L--MVAEP 645
OY 445 LTIIGMIMASAFLEFNINRNQKLIKMSPPYNNLIIIGMLSYASIFLGLDGSFVSEK 504
DB 646 G-AAVCAARFLGLGTLTSLYSALLTKTNRIYRIFEQGRSVTPPPISPTLSQVTFSS 704
OY 505 TFEITCTYRTMILVGYTATGAMFAKTRVHAIFKNVK--MKKK-IIRKQKLIIVYVGM 561
DB 705 TSLQVGMIAVLNAGRPVSHVD-YE-EORTYDPEQA-RGVLK-CDMSDLSL-IGCL-GY- 757
OY 562 LLIDICILICQAVDPLRTRVEKYSMEPPPARDRDISIRPLEHCNTHMTWIGIYAAK 621
DB 758 SLLMWTG-TVYAIKRGVPEPTEAKPIGFTWYTCIWLAFIPDFGTAQSAEKIYIQ 816
OY 622 GILMFGCFLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIIGAIVSLTRDQPNVQFC- 679
DB 817 TTTTLVSLSLASVSLGMLYMPKVYIILFPEONPKRK 855
OY 680 IVALVT-I-FCSTITLCIVFVPRKLITLRNPDAATQNR 716

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RESULT 11

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ID R72095 standard; Protein: 481 AA.
AC R72095;
DR 26-SEP-1995 (first entry)
DE Human mglur7 clone cmr5.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KW signal transducer.
OS Homo sapiens.
PN W09508627-A.
PD 30-MAR-1995.
PF 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PA 19-AUG-1994; GB-016553.
PA (CIBA) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettner I;
DR WPI; 95-139596/78.
DR N-PSDB; Q89345.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PT cpts. which modulate signal transduction activity
PS Claim 8; Page 69-72; 110pp; English.
CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA
CC clones were isolated from cDNA libraries using a rat mglur4 probe.
CC Fetal brain partial cDNA clone cmr5, encoding the protein given in
CC R72095, was obtained. The missing 5' region of the clone was
CC generated by PCR from brain cDNA. Sequence comparison of fetal
CC brain and hippocampus clones indicated the existence of 2 subtypes
CC of hmglur7 (R72097-98).
SQ Sequence 481 AA;

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Query Match 3.3%; Score 214; DB 1; Length 481;
 Best Local Similarity 22.9%; Pred. No. 1.25e-06;
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

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DB 172 LAMGII-ATIFMAFIRYNDPIYRASGRSLVLLTGIFLYC--ITTF-L--MIA- 223
OY 445 LTIIGMIMASAFLEFN--IKNRNOKLIKMSPPYNNLIIIGMLSYASIFLGLDGSFVSE 503
DB 224 KPDVAVCSFRVFLGMCISYVALLTKTNRIYRIFEQGRSVTPARLISPTSLATISS 283
OY 504 KTFETLCYVTRMILVGYTATGAMFAKTRVHAIFKNVK-K--KIIRKQKLIIVYVGM 560
DB 284 LISVOLLGVRI-FEGVDPRNIID-YD-BHKYMNDEQA-RGVLK-CDTIDLOI-ICSL-G 336
OY 561 MLULDL-CILICQAVDPLRTRVEKYSMEPPPARDRDISIRPLEHCNTHMTWIGIYTA 619
DB 337 YSILMW-TC-TVYAIKRGVPEPTEAKPIGFTWYTCIWLAFIPDFGTAQSAEKLY 394
OY 620 YKGLMFGCFLAMETRNVSIPA-LNDSKYIGMSVYVNGIMCIIIGAIVSLTRDQPNVQF 678
DB 395 IQTTTLISMNLSASVALGMLYMPKVYIILFPEONPKRKSF 438
OY 679 C-IVALVT-I-FCSTITLCIVFVPRKLITLRNPDAATQNR 719

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RESULT 12
ID R72093 standard; Protein: 867 AA.
AC R72093;
DR 26-SEP-1995 (first entry)
DE Human mglur7 clone cmr2.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KW signal transducer.
OS Homo sapiens.
PN W09508627-A.
PD 30-MAR-1995.
PF 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PA 19-AUG-1994; GB-016553.
PA (CIBA) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettner I;
DR WPI; 95-139596/78.
DR N-PSDB; Q89343.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying

```


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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 17:26:20 ; Search time 2783.46 Seconds
(without alignments)
-3079.517 Million cell updates/sec

Title: US-09-211-755-3
Perfect score: 2823
Sequence: 1 ATGGCTTCCCGCGAGCTC.....TCATGCTCTCGGCGCTGTAG 2823
Scoring table: IDENTITY_NUC
Searched: 821193 seqs, -1518192014 residues
Database : GenEmbl.*
Word size : 0
Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_ba4:*
5: gb_ba5:*
6: gb_ba6:*
7: gb_ba7:*
8: gb_ba8:*
9: gb_ba9:*
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41: gb_ba41:*
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43: gb_ba43:*
44: gb_ba44:*
45: gb_ba45:*
46: gb_ba46:*
47: gb_ba47:*
48: gb_ba48:*
49: gb_ba49:*

50: gb_pl3:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2823	100.0	2823	12	AF074482	AF074482 Rattus no
2	2816.6	99.8	3288	12	AF109405	AF109405 Rattus no
3	2816.2	99.8	5459	12	AF058795	AF058795 Rattus no
4	2805.2	99.4	5614	12	RN0011318	AF011318 Rattus no
5	2348.2	83.2	5786	11	AF056085	AF056085 Homo sapi
6	2346.6	83.1	2826	10	HS012188	AF012188 Homo sapi
7	2346.6	83.1	2826	40	AF074483	AF074483 Homo sapi
8	2346.6	83.1	3240	40	AF095784	AF095784 Homo sapi
9	2345	83.1	3075	40	AF069755	AF069755 Homo sapi
10	2345	83.1	3155	40	AF099033	AF099033 Homo sapi
11	486.4	17.2	740	11	AF095724	AF095724 Homo sapi
12	415	14.7	743	11	AF095723	AF095723 Homo sapi
13	410.2	14.5	3989	35	AF145639	AF145639 Drosophila
14	347	12.3	2928	9	HS025029	AJ225029 Homo sapi
15	347	12.3	2535	10	HS012186	AJ012186 Homo sapi
16	346	12.3	4281	9	HS012288	AJ012288 Homo sapi
17	346	12.3	4445	9	HS025028	AJ225028 Homo sapi
18	346	12.3	2886	10	HS012185	AJ012185 Homo sapi
19	346	12.3	2700	10	HS012187	AJ012187 Homo sapi
20	346	12.3	3192	40	AF099148	AF099148 Homo sapi
21	342.4	12.1	3202	12	AB016161	AB016161 Rattus no
22	341.8	12.1	4220	9	HS025029	Y10370 R. norvegicus
23	341.8	12.1	2535	12	RN0011318	Y10369 R. norvegicus
24	339.6	12.0	2883	12	RN0011318	AF114168 Mus muscu
25	337	11.2	4365	12	AF114168	AB016160 Rattus no
26	255	9.0	3000	12	AB016160	AC007800 Homo sapi
27	175.4	6.2	153726	33	AC007800	AC011957 Homo sapi
28	168.4	6.0	153790	42	AC011957	AB015334 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS Rattus norvegicus GABA-B receptor 2 (GABA-BR2) mRNA, complete cds.
ACCESSION AF074482
VERSION AF074482.1 GI:4107510
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2823)

AUTHORS	Jones, K.A., Borowsky, B., Tamm, J.A., Craig, D.A., Durkin, M.M., Dai, W., Iac, W.-J., Johnson, M., Gunwaldsen, C., Huang, L.-Y., Tang, C., Shen, Q., Salon, J.A., Morse, K., Laz, T., Smith, K.E., Nagarathnam, D., Noble, S.A., Branchek, T.A. and Gerald, C.
TITLE	GABA(B) receptors function as a heteromeric assembly of the subunits GABA(B)R1 and GABA(B)R2
JOURNAL	Nature 396 (5712), 674-679 (1998)
MEDLINE	99087320
REFERENCE	2 (bases 1 to 2823)
AUTHORS	Borowsky, B., Laz, T. and Gerald, C.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUN-1998) Department of Molecular Biology, Syntactic Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652, USA
REFERENCE	3 (bases 1 to 2823)
AUTHORS	Borowsky, B., Laz, T. and Gerald, C.
TITLE	Direct Submission
JOURNAL	Submitted (06-JAN-1999) Department of Molecular Biology, Syntactic Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652, USA
REMARK	Sequence update by submitter
COMMENT	On Jan 7, 1999 this sequence version replaced gi:4038341.
FEATURES	Location/Qualifiers
source	1..2823

REMARK
COMMENT
FEATURES
source

Sequence update by submitter
On Jan 7, 1999 this sequence version replaced gi:4038341.

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BASE COUNT
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Dd	61	CGCCGTCTCTCTCCCCTTGCTGCTGTGCTGCTGTGTGTGGGCCCGCGGGGCGCTGGGGC	120			
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Db	241	GAGCTAGGCATGAGACAGATCCGACAGACATCTCTGGGCCCTTACTTCTGTGGACCTG	300
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RESULT 2
AF109405 3288 bp mRNA 07-JAN-1999
LOCUS AF109405 3288 bp mRNA 07-JAN-1999
DEFINITION Rattus norvegicus GABA-B receptor 2 mRNA, complete cds.
ACCESSION AF109405
VERSION AF109405.1 GI:4107514
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
1 (bases 1 to 3288)
Kuner,R., Kohr,G., Grunewald,S., Eisenhardt,G., Bach,A. and
Kornau,H.-C.
TITLE Role of heteromer formation in GABAB receptor function
JOURNAL Science 283 (5398), 74-77 (1999)
MEDLINE 99102694
REFERENCE 2 (bases 1 to 3288)
AUTHORS Kuner,R., Koehr,G., Grunewald,S., Eisenhardt,G., Bach,A. and
Kornau,H.-C.
TITLE Direct Submision
JOURNAL Submitted (25-NOV-1998) Department of Neuroscience, BASF-LYXX
Bioscience AG, Im Neuenheimer Feld 515, Heidelberg D-69120, Germany
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REFERENCE
1 (bases 1 to 5459)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 5459)	Clark, J.C., Lam, A. and Bonner, T.I	gb2, A second GABA-B receptor

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 5459)
AUTHORS	Clark, J.C., Lam, A. and Bonner, T.I

TITLE Direct Submission
Submitted (09-APR-1998) Section on Genetics, NIMH, Bldg. 36, Rm
JOURNAL 3D06, MSC 4094, Bethesda, MD 20892-4094, USA

FEATURES	Location/Qualifiers
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ORIGIN

Query Match	99.8%	Score 2816.2	DB 12	Length 5459
Post Local Similarity	99.9%			
Pred	No	0		

Best local similarity	35.0%	freq. no. of	
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		Mismatches	4;
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[illegible]

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DEFINITION Rattus norvegicus mRNA for GABA-B R2 receptor.
ACCESSION AV011318
VERSION AV011318.1 GI:4029344
KEYWORDS gaba-B R2 gene; GABA-B R2 receptor.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 5614)
AUTHORS Kaupmann, K.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1998) Kaupmann K., TA Nervous System, Novartis
Pharma AG, K-125.6.20, CH-4002 Basel, SWITZERLAND
2 (bases 1 to 5614)
AUTHORS Kaupmann, K., Malitschek, B., Schuler, V., Heid, J., Frieestl, W.,
Beck, P., Mosbacher, J., Bischoff, S., Kulik, A., Shigemoto, R.,
Karschin, A. and Bettler, B.
TITLE GABA(B)-receptor subtypes assemble into functional heteromeric
complexes
JOURNAL Nature 396 (6712), 683-687 (1998)
MEDLINE 99087322
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BASE COUNT 1374 a 1664 c 1436 g 1140 t
ORIGIN

Query Match 99.4%; Score 2805.2; DB 12; Length 5614;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2820; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

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LOCUS Homo sapiens GABA-B receptor mRNA, complete cds.
DEFINITION AF056085
ACCESSION AF056085.1 GI:3719225
VERSION
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euarcharia; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5786)
AUTHORS Clark,J.C., Lam,A. and Bonner,T.I.
TITLE gB2, a second GABA-B receptor
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 5786)
Clark,J.C., Lam,A. and Bonner,T.I.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-1998) Section on Genetics, NIMH, Bldg 36, Rm
3D06, MSC 4094, Bethesda, MD 20892-4094, USA

FEATURES
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polya_signal
polya_signal
polya_site
BASE COUNT 1415 a 1670 c 1474 g 1227 t
ORIGIN

Query Match 83.2%; Score 2348.2; DB 11; Length 5786;
Best Local Similarity 89.7%; Pred No. 0;
Matches 2534; Conservative 0; Mismatches 288; Indels 3; Gaps

1 ATGCGTCCCCCGGCAGACTCCGGGAGAGCCCCCGGCGCGCGCGCGCG--CCGCGCGCC 57

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 DB 1838 TCCGAGCCACCCAGAGACCACTTCTGGGGTCCAGGCTCAAGTGTGTTCCGGAAACGG 1897
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 DB 2798 AACCGGCGAGCAGTCAAGCTCTGAGAGGACTGACAGTCAAGAAACCCAGCTTGAATG 2857
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RESULT 6
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 LOCUS HSA012188 2826 bp mRNA PRI 24-APR-1999
 DEFINITION Homo sapiens mRNA for GABAB receptor, subunit 2.
 ACCESSION AJ012188
 VERSION AJ012188.1 GI:3776097
 KEYWORDS GABAB receptor; gabab-R2 gene; subunit 2.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 2826)
 AUTHORS White, J.H., Wise, A., Main, M.J., Green, A., Fraser, N.J., Disney, G.H.,
 Barnes, A.A., Emson, P., Foord, S.M., and Marshall, F.H.
 Heterodimerization is required for the formation of a functional
 GABA(B) receptor
 NATURE 396 (6712), 679-682 (1998)
 JOURNAL MEDLINE 99087321
 MEDLINE 2 (bases 1 to 2826)
 REFERENCE Fraser, N.J.
 AUTHORS Direct Submission
 TITLE Submitted (16-OCT-1998) Fraser N.J., Receptor Systems, Cellular
 Sciences, GlaxoWellcome, Medicines Research Centre, Gunneils Wood
 Road, Stevenage, Herts. SG1 2NY, U.K.
 JOURNAL location/Qualifiers
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D 2581 AATCCCAAGCTCCAGTGAAGACAGAGAGCCCTCTTGAAGATGCAAGAAAGCTATAGAA 2640
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Q 2758 CCAAGCGGAGCGGCTGCGACAGACAGACACCTCTCCAGTATGATGCTCGGGC 2817
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RESULT 7
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LOCUS AF074483 2826 bp mRNA PRI 07-JAN-1999
DEFINITION Homo sapiens GABA-B receptor 2 mRNA, complete cds.
ACCESSION AF074483
VERSION AF074483.1 GI:4107511
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 2826)
AUTHORS Borowsky, B., Laz, T. and Gerald, C.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Department of Molecular Biology, Synaptic
Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,
USA

REFERENCE 2 (bases 1 to 2826)
AUTHORS Borowsky, B., Laz, T. and Gerald, C.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1999) Department of Molecular Biology, Synaptic
Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,
USA

REMARK
COMMENT Sequence update by submitter
FEATURES On Jan 7, 1999 this sequence version replaced gi:4038343.
location/Qualifiers
1..2826

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ORIGIN

Query Match 83.1%; Score 2346.6; DB 40; Length 2826;
Best Local Similarity 89.7%; Pred. No. 0;

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QY	2458	GAGAGACACATACATCAAAAGATCACTACCAAGAGCTCAAGAGATCCTCAAGCTTG	2517
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QY	2578	AACCCCGAGCTCCAGTGGAAACGACAGACGCCCTCAAAACATGCAAAAGACCCATGAA	2637
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QY	2638	GACATCAACTCCCGGAGACACATCCAGCGCGGCTGTGCTCAGCTCCCATCTCTTAC	2697
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DEFINITION	Homo sapiens GABA-B receptor R2 (GABBR2) mRNA, complete cds.		
ACCESSION	AF095784		
KEYWORDS	GI:4836217		
ORGANISM	human.		
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1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
2	(bases 1 to 3240)		
3	Liu,M., Parker,R., McCreia,K., Watson,J., Baker,E., Sutherland,G. and Herzog,H.		
4	Cloning and characterization of a novel human GABA-B receptor subtype with high affinity for GABA and low affinity for baclofen		
5	Unpublished		
6	2 (bases 1 to 3240)		
7	Liu,M., Parker,R., McCreia,K., Watson,J., Baker,E., Sutherland,G. and Herzog,H.		
8	Direct Submission		
9	Submitted (15-NOV-1998) Neurobiology Program, Garvan Institute of		
10	Medical Research, 384 Victoria St, Sydney, NSW 2010, Australia		
11	Location/Qualifiers		
FEATURES			

[illegible]

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Oy	838	ATCCCGGAGATGATGACAGCCTCGCTGTGTGGGAG	CGAGTGTGAGAGGCAATTCCTCA	897
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[illegible]

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RESULT 10
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DEFINITION mRNA, complete cds.
ACCESSION AF099033
VERSION AF099033.1 GI:5639666
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3155)
Martin,S.C., Russek,S.J. and Farb,D.H.
Molecular identification of the human GABABR2: cell surface
expression and coupling to adenylyl cyclase in the absence of
GABABR1
Mol. Cell. Neurosci. 13 (3), 180-191 (1999)
JOURNAL MEDLINE
99263199
REFERENCE 2 (bases 1 to 3155)

AUTHORS Martin,S.C., Russek,S.U. and Farb,D.H.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1998) Laboratory of Molecular Neurobiology,
Department of Pharmacology, Boston University School of Medicine,
715 Albany Street, L606, Boston, MA 02118-2394, USA

FEATURES
Source Location/Qualifiers

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variation

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 VERSION AJ012186.1 GI:3776093
 KEYWORDS GABAB receptor; gabab-R1 gene; subunit 1b.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2535)

GenCore version 4.5
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OM nucleole - nucleole search, using sw model

Run on: March 16, 2000, 17:40:53 ; Search time 151.92 Seconds

(without alignments)
4649.106 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database: N_Geneseq_36.*

Word size: 0

Number of hits that pass the threshold: 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	346	12.3	2620	1	V10265	Human GABA-BR1a/b
3	342.4	12.1	2837	1	V10266	Rat GABA-BR1a rece
4	339.6	12.0	4376	1	V10264	Rat GABA-BR1a rece
5	241.6	8.6	314	1	V88919	EST clone HM456. N
6	143.4	5.1	361	1	X51891	Human secreted pro
7	63.4	2.2	1028	1	Q27091	XYT26 probe. DNA s
8	59.8	2.1	10596	1	V51731	Plasmid pcISBON f
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18	55	1.9	3109	1	O24952	DNA induced in hum
19	55	1.9	3132	1	V64276	Human EBR-1 CDNA.
20	54.8	1.9	11820	1	V81830	Human chromosome 1
21	54.6	1.9	1089	1	N92576	Sequence of the 1.
22	54.6	1.9	1089	1	T93593	Elmeria tenella sp
23	53.4	1.9	5011	1	O65377	Multidrug resistan
24	53.4	1.9	5011	1	T37173	CDNA encoding mult
25	53.4	1.9	4834	1	T14912	CDNA encoding mult
26	53.4	1.9	4864	1	T14911	CDNA encoding mult
27	53.4	1.9	4423	1	T14914	CDNA encoding mult
28	53.4	1.9	4885	1	T14910	CDNA encoding mult
29	53.4	1.9	4669	1	T14913	CDNA encoding mult
30	53.4	1.9	5011	1	V31497	Human multidrug re
31	53.4	1.9	5011	1	V31498	Human MDR variant
32	53.4	1.9	5011	1	X21977	Human MDR variant
33	53.4	1.9	5011	1	X21976	Human multidrug re
34	53.4	1.9	5011	1	X19817	Human multidrug re
35	53.4	1.9	5011	1	X19818	Human multidrug re
36	52.2	1.8	397	1	X51965	Human secreted pro
37	51.4	1.8	954	1	N90505	DNA encoding Group
38	51.4	1.8	957	1	V66836	Group B Elmeria te
39	51	1.8	678	1	V23145	5' fragment of Rat

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB	ID	Description
1	V10267	347	12.3	2924	1	V10267	Human GABA-BR1b re
2	V10265	346	12.3	2620	1	V10265	Human GABA-BR1a/b
3	V10266	342.4	12.1	2837	1	V10266	Rat GABA-BR1a rece
4	V10264	339.6	12.0	4376	1	V10264	Rat GABA-BR1a rece
5	V88919	241.6	8.6	314	1	V88919	EST clone HM456. N
6	X51891	143.4	5.1	361	1	X51891	Human secreted pro
7	Q27091	63.4	2.2	1028	1	Q27091	XYT26 probe. DNA s
8	V51731	59.8	2.1	10596	1	V51731	Plasmid pcISBON f
9	T40348	59.8	2.1	10596	1	T40348	Plasmid pcISBON f
10	V21683	59.8	2.1	9600	1	V21683	Vector plasmid pcm
11	V58531	59.8	2.1	799	1	V58531	Nucleotide sequenc
12	X15650	59.8	2.1	10596	1	X15650	Nucleotide sequenc
13	T36035	58.6	2.1	6407	1	T36035	rchd528 gene diffe
14	V81825	58.6	2.1	6407	1	V81825	Human rchd528 enco
15	X26245	58.6	2.1	6407	1	X26245	CDNA sequence of r
16	O79630	57.4	2.0	2974	1	O79630	Partial FRAXE regi
17	V55830	57	2.0	795	1	V55830	FLGA insert stabl
18	O24952	55	1.9	3109	1	O24952	DNA induced in hum
19	V64276	55	1.9	3132	1	V64276	Human EBR-1 CDNA.
20	V81830	54.8	1.9	11820	1	V81830	Human chromosome 1
21	N92576	54.6	1.9	1089	1	N92576	Sequence of the 1.
22	T93593	54.6	1.9	1089	1	T93593	Elmeria tenella sp
23	O65377	53.4	1.9	5011	1	O65377	Multidrug resistan
24	T37173	53.4	1.9	5011	1	T37173	CDNA encoding mult
25	T14912	53.4	1.9	4834	1	T14912	CDNA encoding mult
26	T14911	53.4	1.9	4864	1	T14911	CDNA encoding mult
27	T14914	53.4	1.9	4423	1	T14914	CDNA encoding mult
28	T14910	53.4	1.9	4885	1	T14910	CDNA encoding mult
29	T14913	53.4	1.9	4669	1	T14913	CDNA encoding mult
30	V31497	53.4	1.9	5011	1	V31497	Human multidrug re
31	V31498	53.4	1.9	5011	1	V31498	Human MDR variant
32	X21977	53.4	1.9	5011	1	X21977	Human MDR variant
33	X21976	53.4	1.9	5011	1	X21976	Human multidrug re
34	X19817	53.4	1.9	5011	1	X19817	Human multidrug re
35	X19818	53.4	1.9	5011	1	X19818	Human multidrug re
36	X51965	52.2	1.8	397	1	X51965	Human secreted pro
37	N90505	51.4	1.8	954	1	N90505	DNA encoding Group
38	V66836	51.4	1.8	957	1	V66836	Group B Elmeria te
39	V23145	51	1.8	678	1	V23145	5' fragment of Rat

PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ:
DR WPI: 98-042183/04.
P-PSDB: W40117.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 3; Page 56-62; 108bp; English.
CC This cDNA sequence encodes a novel human GABA-B receptor protein,
CC GABA-B1a/b. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 2620 bp; 593 A; 716 C; 710 G; 601 T;

Query Match 12.3%; Score 346; DB 1; Length 2620;

Best local Similarity 50.6%; Pred. No. 8, 6e-60;

Matches 1037; Conservative 0; Mismatches 975; Indels 36; Gaps 7;

QY 217 GGGCGGGCGCTGCTCCCCCGCTGGAGCTAGCCATGAGCA---GATCCGCAACGAGTCA 273
DB 49 GGGCAGGCGCTGGCAGCGCGCGTGAGAGTGGCGCTGAGAGCACTGATATACGAGGAC 108
QY 274 CTCTGCGCGCCCTACTCTCTGAGACTGCGACTATGACACCGAGTGAATGCAATGCAAG 333
DB 109 ATCTGCGCGAGCTATGAGCTCAAGCTCATCCACGACGACGAAGTGTGATCCAGGCGAA 168
QY 334 GGAATGAAGCCTTCTATGAGCAATTAAGTATGAGCGCGCAATTTGATGTTTGA 393
DB 169 GCCACCAAGTACATATGAGCTGCTTACAGACCCCTATCA--GATCATCTTTATG 225
QY 394 GGGCTGTGCTGTGTGTCACATCTATATGGCGAGTCCCTCCAGGCTGGATGCTG 453
DB 226 CTTGGCTGACAGCTGTGTCTCAGCGCTGTGAGGCTCTGAGATGTGAACCTCAT 285
QY 454 CAGCTTCTCTGCGCGCACACGCTGTTCTTGGGATGAAGAAGTACCCGATTTTC 513
DB 286 GTGCTTCTCTATGCTGCTCAGCTCAGCCCTGTCAAAACGGGAGGCTTTCCCATCTTC 345
QY 514 TTCCGAGCGGTGCGTCAAGACACGCGGTGAACCCGCTCATCTGAAGCTCTGAAAC 573
DB 346 TTCCGAAGCGCACCCATCAGCCACTCCACAAACCTACCCGCGTGAACCTTTGAAAG 405
QY 574 TTCCGCGTGGCGGTGGGGGACACATCAGCAGGACGCGCTTCTCCGAGTGAAG 633
DB 406 TGGGCTGTGAAGAAGATTGCTACATCCAGCAGACATGAGTCTTACCTTGCACCTG 465
QY 634 AATGACCTGACTGGGGTCTGTATGGGAGATATTTGATCTCAGACACAGAGATTTTC 693
DB 466 GACGACCTGTGAAGACGATGAAAGAGGCTGAATTTGATTTCCGCGCAAGTTTC 525
QY 694 TCCATATGCTCCGTGACACAGCTCAAAAAGCTCAAGGGAATGACGTGCGGATATCCT 753
DB 526 TTCTCAGATCCAGCTGTCCTCCGTCAAAACCTGAAGCGCCGAGATGCCGATATCTG 585
QY 754 GGGCAGTTTGAAGATATGAGCAGCAAAAGCTCTTCTGTTGCTTGCAGAGAGCATG 813
DB 586 GGAATTTCTATGAGACATGGAAGCGCGGAAAGTTTGTGAGGTGTACAAAGAGGCTTC 645
QY 814 TTGGCAGCAAGTACCATGATGATCTCCCGGATGCTGACAGCCGCTGCTGGAGAG 873
DB 646 TTGGGAGAAAGTACGTGTGTTCTCTCATTTGGGTGTGATGTCGACAAATTTGTAAGA-- 704
QY 874 GTGCAATGTGGAAGCCATTTCTCAGCGTGCCTGGCAGAAAGCCTCTGCTGCCATGGA 933

DB 704 -----TCTACGACCTTCTATCAACTGCACAGTGAATGAGTACTAGCGCGGTGAG 756
QY 934 GGTATATCGAGTGGACTTTGAGCCCTGAGGCTCCAAACAAATCAAGACATCTCAGG 993
DB 757 GGGCATTCTCACTGAGATGATGCTGATATCTGATCTGATCTGATCTGATCTGATCTG 816
QY 994 AAGATCTCAGACAGTATGTAAGAAGATACACAGCAAAAGCTTCAAG-----CGTGGG 1047
DB 817 ATGATCTCCAGGAATTTGTGAGAAATTAACCAACGACGATGAAAAGACACCTGAGAG 876
QY 1048 CCCAGCAAGTTCCATGGGTACCGGCTACGATGGATCTGGGCTATCGCCAAAGACCTCAAG 1107
DB 877 ACAGAGGCTTCCAGAGGACCGCTGCTATGATGCTATGCTGCTGCTGCTGCTGCTG 936
QY 1108 AGGCGATGAGACATGATGCTAGTACGAGCAGCAGCGGATCCAGGACTTCAACTAC 1167
DB 937 CTGAACCAAGATCTGAGAGGAGGCGCGCTTGTGTGCTGCTGCTGCTGCTGCTGCTG 996
QY 1168 ACAGACACAGCTGGGCAAAATATCTCTCAATGCCATGAACGACGACCACTTCTGCGG 1227
DB 997 AACAAACGACCATTTACCGACCAAAATCTACCGGCAATGAACCTTGTCTTTGAGGT 1056
QY 1228 GTACGCGGTCAAGTTGTTGTT---CCGAGCGGGAGAGAAATGGGAACCATTAATTTACT 1284
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QY 1285 CAATTTCAAGACAGCAGAGAGTGAAGTGGCGAATACACGCGGTGCTGACACACTG 1344
DB 1117 CAGCTTCAAGGTGGAGAGTACAAAGATTTGGTACTATGACACACCAAGAGATGATCTT 1176
QY 1345 GAGATATCAATGACACATTAAGTTTCAAGGGTCCAGCCACCAAGGACAAAGCATC 1404
DB 1177 TCTGTGCTCAAAACAGATTAATGATGAGAGGTGCCCCCAGC---TGACACAGCCTG 1233
QY 1405 ATTGTGAGCAGCTTCGGAAGATCTCGCTTCCAGTATGACATCTGTCGCTGCTAC 1464
DB 1234 GTATCAAGACATTCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1293
QY 1465 ATCTGCGCATGATGATGAGCGAGCGCTCTCTCTTCTTCAACATCAAGAACCGGACCA 1524
DB 1294 AGCTGGGAGTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1353
QY 1525 AAGCTGATTAAGATGTCAGAGCCCTACATGAACCAACCTACATGCTGGAGAGATG 1584
DB 1354 CGTTATATCAAGACTCAAGCGCCCAACCTGAACACATGCTGCTGCTGCTGCTGCTG 1413
QY 1585 TCCATATGATCCATCTCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1644
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QY 1645 GAAACATCTGCAAGGTCGCGACCTGATCTCAACGCTGGGCTACACAACTGCCCTTGG 1704
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QY 1705 GGCATGTTTGCAAAAGCTGAGGAGGCTCATGCTGCTTCAAAATGTAAGATGAAGA- 1764
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DB 1654 ATGATGTCTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713
QY 1876 AGGTACAGATGAGCGCGAGCCAGCGAGCGGACATCTCCATCCGCCATTTGCTGGA 1935
DB 1714 ACATTTGCCAAGAGGAACCTTAAGAAATATTGAGCTGTATTTCTGCCCAGCTGGAG 1773
QY 1936 CACTGCAAAACACCAATGACATCTGCTTGGATTTGCTTACGCTTCAAGAGGGCTC 1995
DB 1774 CATTTGAGCTCCAGGAAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1833

QY 1996 CTCATGCTATGCTGTTCTTGGACGGAACCCCAATGATGATCCCTCCCTC 2055
 DB 1834 CTGCTCTGCTGATCTCTTCTTATGACCAAGAGTGTCCACTGAGAAATG 1893
 QY 2056 AAGGACAGAGACATGAGTGTGATGATGATGATGATGATGATGATGATG 2115
 DB 1894 AATGATACACCGGCTGTGGCATGCTATCAATGATGATGATGATGATGAT 1953
 QY 2116 GCTGCTGCTCTCTCTGACGCGTACAGCCCAAGTGTGATGATGATGATG 2175
 DB 1954 GCTCTGATCACCATGATGATGATGATGATGATGATGATGATGATGATG 2013
 QY 2176 GATATATCTTGTGACGACACATCTCTGCTGCTGCTGCTGCTGCTGCT 2235
 DB 2014 GCCATGTTCTCTCTCTATATCACTTGTGCTGCTGCTGCTGCTGCTGCT 2073
 QY 2236 CTGAGGAC 2243
 DB 2074 CTGATCAC 2081
 RESULT 3
 VI0266
 ID VI0266 standard; cDNA to mRNA; 2837 BP.
 AC VI0266;
 DT 03-JUN-1998 (first entry)
 DE Rat GABA-BR1b receptor cDNA.
 KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;
 inhibitory neurotransmitter; peripheral nervous system; antagonist;
 treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
 KW epilepsy; cognitive function; ds.
 OS Rattus norvegicus.
 FH Key Location/Qualifiers
 FT CDS 228..2762
 FT /tag= a
 FT /product= GABA-BR1b
 PN WO9746675-A1.
 PD 11-DEC-1997.
 PF 19-MAR-1997; E01370.
 PR 22-NOV-1996; US-756091.
 PR 30-MAY-1996; US-655716.
 PA (NOVS) NOVARTIS AG.
 PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Michel SJ;
 DR WPI; 98-042183/04.
 DR P-PSB; M40118.
 PT Purified GABA-B receptor or receptor protein - and antagonists of
 PT these which may be useful in treating nervous system disorders
 PS Claim 3; Page 67-74; 108PP; English.
 CC This cDNA sequence encodes a novel rat GABA-B receptor protein.
 CC GABA-BR1b (gamma-aminobutyric acid) is the major inhibitory
 CC neurotransmitter found in the brain and peripheral nervous system
 CC and this receptor may be used for the identification of GABA-B
 CC receptor agonists and antagonists. Such proteins may be used in
 CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
 CC bronchial inflammation or asthma or to improve cognitive function.
 CC GABA-B receptor ligands and probes derived from this sequence can be
 CC used to assay for GABA-B receptors or DNA encoding them
 SQ Sequence 2837 BP; 621 A; 842 C; 764 G; 610 T;

Query Match 12.1%; Score 342.4; DB 1; Length 2837;
 Best Local Similarity 49.7%; Pred. No. 4.5e-59;
 Matches 1128; Conservative 0; Mismatches 1091; Indels 51; Gaps 8;

QY 130 GAGCCCCCGGCGCCGACAGCCGCGCTCTCATCTATGAGGCTCATGCCCTC 189
 DB 327 CATCCCGCGCGCTCACCAGAGGCTCCCCCACCCTCTCTCAAGAGGGGTGAGTA 386
 QY 190 ACCAAGAGTGGCCAGAGGAGAGTGGGCGC-----GGCGTGGCGCC 234
 DB 387 TACATGCGGCGCTGTTTCCATGAGCGGGGCTGGCCGGGGGCGAGCTGCCAGCC 446
 QY 235 GCGGTGAGCTAGCCATGAGCA--GATCCGACAGAGTCACTCTGCGCCCTACTTC 291
 DB 447 GCGGTGAGATGGCGCTGAGAGCTTAAACGCGGAGAGATCTCTGCGGACTACGAG 506
 QY 222 CTGAGCTGGACACTCTATGACACCGAGTGTGACAAATGCAAGGAGATGAACTTTAT 351
 DB 507 CTCAAGCTTATCCACACAGACAGAGTGTGACCCAGGAGACCCCAAGTACTGTGAC 566
 QY 352 GACGCAATTAAGTATGGCGGAGAACCATTTGATGATGATGATGATGATGATGAT 411
 DB 567 GAATCTCTTCAATGACCCCATCAAGATCATCTCATGCTG--CTGATGTTCTGTC 623
 QY 412 ACATCTATATGCGGAGTCCCTCCAGGCTGGAATCTGTGAGCTTCTGCGCCGCG 471
 DB 624 TCCACACTTGTAGCTGAGGCTCCCGGATGTGAACTTATGCTCTCATATGAGCTCC 683
 QY 472 ACCAGCCTGTTCTTGGGATTAAGAAAGTATACCCGATTTCTCCGAGGCTGCTCA 531
 DB 684 AGTTCAACAGCCTTGTCAAAACCGACGGCTTCCACGTTCTCCGAGCATCATC 743
 QY 533 GACAAAGCGGTGAACCCCGCATCTTAAGCTCTGAAGACCTCCGCTGGCGGTG 591
 DB 744 GCACACTTCACAAATCCACCCCGGTTGAAACTTTCGAAAGGGGCTGGAAGATG 803
 QY 593 GGCACACTCAGCAGAGAGTGTGACGCTTCCGAGGTGAGATGATGATGATGATGAT 651
 DB 804 GGTACATTCACACAGACACCGAGGCTTCCACCTCAAGCTGATGATGATGATGATG 863
 QY 653 CTGTATGGGGAATATGAGATCTCAGACACAGAGATTTCTCCATATATCCCTGAC 711
 DB 864 GTGAAGAGGCTGGATCGAATCATCTTCCGACAGATTTCTTCGATGATGATGATG 923
 QY 712 AGCTCAAAAGCTCAAGGGAATGAGTGTGATGATGATGATGATGATGATGATGAT 771
 DB 924 CCGTTTAAACCTGAAAGCTCAAGATGCTGATATGATGATGATGATGATGATGAT 983
 QY 772 ATGCAAGCAAAAGCTTCTGTTGCTTGGCTGAGAGAGATGTTTGGACAGCAATGAC 831
 DB 984 GAAGCCCGGAAAGTTTGTGAGGCTTATAGAAAGGCTTGTGGAGAAAGTACGTC 1043
 QY 832 TGATCATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891
 DB 1044 TGGTCTCTATCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1103
 QY 892 TCTTACGCTGCTGCGAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
 DB 1104 TGTAAAGT-----GGAAGAAATACCGAGCGGTGAGGCGCACATCCACAGGAG 1154
 QY 952 TTGAGCCCTGAGCTCCAAAGCAATCAAGACATGCAAGAGAGCTCAACAGCATAT 1011
 DB 1155 ATTGTCATGCTGAACCTTGGCCACACCCGAAGATTTTCCAACTGACGTACAGAAATTT 1214
 QY 1012 GAAGAGAGTACAAAGC-----AAAGTTCAAGCGGTGGGCGCCAGCAATTCATGG 1065
 DB 1215 GTGAGAAACTTAACCAAGCGCTGAAGAACACCCGAGAGACTGAGAGCTTCCAGAG 1274
 QY 1066 TACGCTACATGAGGATCTGATGATGATGATGATGATGATGATGATGATGATG 1125
 DB 1275 GCACACTGCGCTTATGATGCTATGATGCTTGTGCTTGTGCTTGTGAACAAGAGTGTGA 1334
 QY 1126 CATGCAATGACAGCAAGCAAGCGATCAGAGCTCAACTACAGACCAACAGCTGGGC 1185
 DB 1335 GAGGTGTGTTCCGCGGTGCTGAGGAGCTTAACTACAAACAGACCAATTACA 1394
 QY 1186 AAATATCTCTCAATGCTCAATGACAGACCAACTTCTTGGGCTCAAGGCTCAAGTTTG 1245

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Db 1395 GACCAGATCTACCGGCGCATGAACTCTCTCTTGAGGCGCTTCTGGCATGTGTCTC 1454
QY 1246 TT---CCGGAGCGGGAGAGAAATGGGAACCATTAATTACTCATTTTCAAGACGAGA 1302
Db 1455 TTGATGATCCAGCGGCTCCCGGATGGATGGACATTATCGAGCAGCTACAGGGCGAGC 1514
QY 1303 GAGGTGAAGGTGGCGAATACAAAGCGGTGGCTGACACACTGGAGATCATGATGACAC 1362
Db 1515 TACAAAGATGCGCTACTACAGACACCAAGATGATCTTCTGCTCCAAAGCGAG 1574
QY 1363 ATAAAGTCCAGGGGTCCGAGCGCCCAAGAGACCATTCCTGGAGCACTCGG 1422
Db 1575 AAGTGAATGGAGGCTC---TCCCGAGCTGACCAAGCTTGTGATCAGACATTCCT 1631
QY 1423 AAGATCTCGCTTCACATGATAGCATCTCTGCTGCTCAGCATCTCGGCGATGATG 1482
Db 1632 TTGCTGTCTAGAACTCTTTATCTCCGCTCAGTTCTCAGCGCTGGGATGTTCTT 1691
QY 1483 GCGAGGCGCTCTCTCTTCTTCAACATCAAGAACCGGAACCAAAAGCTGATTAAGATCA 1542
Db 1692 GCTGTGTCTGTCTGCTTAAACATCAACATCCCAAGTTCGTTATATCCAGACTTC 1751
QY 1543 AGCCCTACATGAAACACATCTCATCTCTGAGGAGAAATGCTCTATGATCCATCTTC 1602
Db 1752 CAGCCCACTGAACATCTGACTGCTGTGGCTGCTCAGTGGCACTGGCTGTCTCTTC 1811
QY 1603 CTCTTTGGCTGATGGGTCTCTGCTCAAGAAAGACTTTGAAACACTGTGACGCTC 1662
Db 1812 CCTCTGGGTGGATGTTACCAATAGGAGAGACCAAGTCCCTTGTCTGCTGACGCTC 1871
QY 1663 CGGACCTGATTTCTACCGTGGCTACACACTGCTTTGGGGCCATGTTTGAAGAAC 1722
Db 1872 CGGCTTTGGCTTTGGGCTTTAGCTGTGGCTATAGGCTATAGTCTACCAAGATC 1931
QY 1723 TGGAGGCTCATCCATCTTCAAAATGTGAAGATGAAGA-----GAAATCATC 1773
Db 1932 TGGGGGTCCACAGATCTTCAAGAAAGAGAGAAAGAAAGATGAGGAAACCTTA 1991
QY 1774 AAGACACAGAGCTGTGATTTGGGGGCGATGCTGCTCATGAGCTGTGATCCTG 1833
Db 1992 GAGCCCTGGAACATCTATGCACTGTGGCTGTGGCTGTGGATGATGATGCTGATCTT 2051
QY 1834 ATCTGTGGCAGGCTGTGACCCCTGCGGAGAGACATGAGAGGTACAGATGAGCGC 1893
Db 2052 GCCATCTGGCAGATTTGGACCCCTTGCACCGAACCATTGAGACTTTGCCAAGGAGAA 2111
QY 1894 GACCCAGCAGGCGGAGCATCTCATCGCCCATGCTGGAGACTTGGAAACACCCAC 1953
Db 2112 CCAGAGAAACATCATGATCTTCAATTTGCCCACTTGGAGCATGCTCAAGAG 2171
QY 1954 ATGACATCTGGCTTGGCATTTGTACGGCTTACAGAGGCTCTCATGTTGGTGT 2013
Db 2172 ATGAAATAGTGGCTTGGCATTTTCTATGTTTACAGAGGCTCTGCTGCTGTGGAAATC 2231
QY 2014 TTCTTGGCATGGAAACCCGCAATGAGATGCCGCCCTCAAGCAGAGAAAGATCATC 2073
Db 2232 TTCTTGTCTTACGAACCAAGAGCGTGTCCACTGAAAGAAATCAATGACACAGGCGCTG 2291
QY 2074 GGCATGAGTGTACATGTGGGATCATGTGCATCATCGGGCTGTCTCTCTCTCTG 2133
Db 2292 GGCATGGCTATCTACATGTGTGGGCTGTGTGTCTCATCTAGTCTGTGACATGATC 2351
QY 2134 AGCGGTGACCAAGCCCAACGTCGATGTGATGTGAGCCCTGTGATCATCTTCTGCAAGC 2193
Db 2352 CTTCAGTGAAGGAGGAGCGAGCTTGTGCTTGTGCTGTGCTGATGCTCTTCTC 2411
QY 2194 AACATCACTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2243
Db 2412 TACATCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2461

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RESULT 4

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V10264
ID V10264 standard; cDNA to mRNA; 4376 BP.
AC V10264;
AT 03-JUN-1998 (first entry)
DE Rat GABA-B1a receptor cDNA.
KW Gamma-aminobutyric acid; GABA-B1a receptor; rat; brain; agonist;
KW Inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function; ds.
OS Rattus norvegicus.
FH Key Location/Qualifiers
FT CDS 182..3064
FT /tag= a
FT /product= GABA-B1a
FT
FT W0974675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bitliger H, Froestl W, Kaupmann K, Mickel SJ.
DR WPI: 98-042183/04.
DR P-PSDB: W40116.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 3; Page 42-50; 108BP; English.
CC This cDNA sequence encodes a novel rat GABA-B receptor protein.
CC GABA-B1a. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them
SQ Sequence 4376 BP; 940 A; 1209 C; 1195 G; 1032 T;

Query Match 12.0%; Score 339.6; DB 1; Length 4376;
Best Local Similarity 50.4%; Pred. No. 1.7e-58;
Matches 1033; Conservative 0; Mismatches 979; Indels 36; Gaps 7;

QY 217 GGGCGGCGGTGTCTCCCGCGGTGAGCTAGCATGAGACA---GATCGCAACAGATCA 273
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QY 274 CTCCTGCGCCCTCTCTCTGAGCTGCGACTCTATGACACGAGTGTGACATCAAG 333
Db 791 ATCTGCGCGACTACGAGCTCAGCTTATCCACAGACAGCAAGTGTGCCAGAGCA 850
QY 334 GGCATGAAGACCTTTATGACGCAATTAAGTATGGCCGAAACCATTTGATGTTTGA 393
Db 851 GCCACCAAGTACTGTACGAACTCTACAAAGACCCCATTAAGATCTTCTCATGCT 910
QY 394 GCGCTCTCCGTCTGACATCTATATGCGGAGTCCCTCAAGCGGAGATGTGGTG 453
Db 911 GGTCTGTCTGTCTGCTGACACTGTGAGCTGTGAGGCTGCCGATGTGGAATCTTAT 967
QY 454 GAGCTTCTCTGCGCCACCGCTGTCTTGTGGGATTAAGAAAGATACCCGATTTTC 513
Db 968 GTGCTCTATATGCTCTCAGTTCACGCTTGTCAAAACGAGAGGCTTCCACAGTTC 1027
QY 514 TTCCGAGAGGTCGCTGACGACCAAGCGGCTGAACCCGCGCATCTGAGAGTCTGAGAC 573
Db 1028 TTCCGAGAGCATTCATCCGACACTCCAAATTCACACCGGCTGAATCTTTCGAAAG 1087
QY 574 TTCCGTCGCGCGGTGTGTGGCACAATGACGAGAGCTGTGAGCGCTTCTCGAGGTGAG 633
Db 1088 TGGGCTGTGAAGAAATGTGATTCATCCAAAGACCAAGAGGTCTTTCACCAACGCTG 1147
QY 634 AATGACTGACTGGGCTTCTGTATGGGGAAGATATGAGATTCACACAGAGAGTTTC 693
Db 1148 GATGACTGTGAGAGGAGCAAGTAAAGAGGCTGGGATGAGATCACTTTCCGAGAGATTTC 1207

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QY 694 TCCATATGTCCTGACACGCGTCAAAAAGCTCAAGGGGATGACGTGGGATCATCTT 753
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1208 TTTCGGATCCAGCTGTGCTCCGTTAAAACCTGAAAGGCTCAAGATCTGAAATCATGG 1267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 754 GGCAGCTTTGACCAAGATATGACGAAAAGCTCTTGTGTGCTGCTCCAGAGAGCATG 813
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1268 GGAATTTCTATGAGAGGAAAGCCGGAAGTTTGTGTAGGTCTATTAAGAAAGGCTC 1327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 814 TTGGCAGACAGTACAGTATGATCCCGGATGTGTACAGGCTGCTGTGTGGAGAGAG 873
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1328 TTGGGAAAGAGTACGTGTGCTCTCATGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 1387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 874 GTGATGTGTGAGAGCCATTTCTCAGCTGCTGCGAGAAAGCCCTGCTGCTGCTGCTG 933
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1388 TATGACCCGCTCAATCAATTTGTACAGTGA-----AATAATGACCGAGGGGGTGGAG 1438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 934 GGTTCATTCGAGAGTGTGATTTGAGCCCTGAGCTCCAAACAAATTCAGACATCTCAGGG 993
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1439 GGCACATCCACCGAGAGATTTGTATGTGTGAAACCTGCGCAACCGCGAAGCATTTTCCAA 1498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 994 AAGACTCCACAGCAGTATGAAGAAGATAGACA-----GCAAGCTTCAGGCGTGGAG 1047
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1499 ATGACGTCAAGGAATTTGTGAGAAACTAACAAGCGGCTGAAAGACACCGCGAGAG 1558
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1048 CCCAGCAAGTTCATGGGTACGCTACGATGGATCTGGGTCTATGCGCAAGACCTCAG 1107
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1559 ACTGAGGCTTCTCAGAGAGGACCACTGCGCTATGATGATCTATGCGCTTGGCTTGGCC 1618
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1108 AGGCGCATGAGACACTGATGCGATGAGCAGCAGCAGCGGATCCAGACATTCATCTAC 1167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1619 TTGAACAAGAGCTGTGAGAGAGTGTGTGCTGCGGCTGCGGCTTGGAGCTTAACTAC 1678
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1168 AAGAGCCACAGGCTGGGCAAAATCATCTCTCATGCTGATGACAGACCAACTCTTCGGG 1227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1679 AACAACCGACCATTTACAGACCAAGATCCGCGCAGTGAATCTCTCTTGAAGGCT 1738
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1228 GTACAGGGTCAAGTTGTGTCGG--AACGGGAGAAATGGGAAACATTAATTACT 1284
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1739 GTTCTGCGCATGTGTCTTGTATGACGCGGCTCCGAGTGAACATGACATTAATCAGAG 1798
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1285 CAATTTCAAGCAGCAGAGAGTGAAGTGGGAGATGACAGCGGAGTGGTGCATACAG 1344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1799 CAGCTACAGGCGGAGCTACAGAAAGATCGCTACTACAGCAGCAGCAAGATGATCTT 1858
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1345 GAGATCATCATGACACCATTAAGTTCCAGGGGTCCGAGCCACCAAGCAAGACCATC 1404
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1859 TCTGTGTCAAAACGACCAAGTGTGAGGCTCTCCCCAGC--TGACAGACCTTG 1915
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1405 ATTCTGAGACAGCTTGGAAAGTCTCGCTTCCATGATATGATCCGTCGCTGCTGAC 1464
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1916 GTTATCAAGACATTCCTGTTCTGTCTTCAAGAACTCTTATCTCCGTCTCAGTTCTCTC 1975
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1465 ATCTCGGAGATCATGAGGCAAGGCTTCTCTCTTCTTCAACATCAAGAACGGAACAA 1524
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1976 AGCTGTGGAGATGTTCTGTCTGTGTCTGTCTGTCTTAACTTCAACTCCACGCTT 2035
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1525 AAGCGATATAGATGTCAAGCCCTACATGAAACAACTCATCTCCAGGAGGATCTG 1584
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2036 CCTTATTCAGAACTCCAGGCGCAACTGAAACATGTGCTGTGTGTGTGTGTGTGTGT 2095
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1585 TCCATGATCATCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2096 GCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1645 GAAACACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1704
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2156 CCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1705 GCGATGTTTGAAGAACTGAGGCTCATGCAATCTTCAAAAATGTGAAGATGAAGAA- 1764
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2216 TCTATGTTTCAACCAAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 1764 -----GAATATCATCAAGACCAAGACAGCTGCTGTGTGTGTGTGTGTGTGTGTGT 1815
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2276 GAGTGTGAGGAGACCTCTAGACCCCTGGAAACTCTATGCACTGTGTGTGTGTGTGTGT 2335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1816 ATGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1875
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2336 ATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1876 AGTACAGATGAGACCGGAGCCAGCAGGCGGAGACATCTCCATCCGCTCATGTGTGAA 1935
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2396 ACTTTTGTGCAAGAGAAACCAAGAGAGACATGATGTCTCATTTCTGCTCCAGTTGGAG 2455
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1936 CACTGTGAAACACCCACATGACATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1995
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2456 CACTGTGATCCCAAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2515
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1996 CTCATGCTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2055
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2516 CTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2575
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2056 AACGACAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2576 AATGACCAACAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2635
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2116 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2636 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2695
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2176 GTTCATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2696 GGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2755
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2236 CTGAGGAC 2243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2756 CTGATCAC 2763
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 5
V88919
ID V88919 standard; cDNA; 314 BP.
AC V88919;
DE 12-FEB-1999 (first entry)
KW EST clone HM456.
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; actinin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
OS Homo sapiens.
PN M09845437-A2.
PD 15-OCT-1998.
PE 10-APR-1998: U06956.
PR 10-APR-1997: US-837312.
PA (GEMT ) GENETICS INST INC.
PI Agostino KJ, Jacobs K, Lavalie ER, McCoy JM, Merberg D,
PI Racie LA, Spaulding V, Treacy M;
DR WPI: 99-070078/06.
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries
PS Claim 1: Page 556-557; 64pp; English.
CC The present sequence represents an expressed sequence tag (EST), and is
CC a polynucleotide of the invention. The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC actinin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene

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CC therapy. 314 BP; 72 A; 81 C; 89 G; 72 T;
SQ Sequence

Query Match 8.6%; Score 241.6; DB 1; Length 314;
Best Local Similarity 87.2%; Pred. No. 2.3e-39;
Matches 265; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1733 ATGCATCTTCAAAATGTAGATGAGAGAAAGATCATCAAGACGAGACTGCTTG 1792
DB 3 ATTCGGCCCTTCATGAGCCATAGAAATGAAAGAAAGATCATCAAGACCAAACTGCTTG 62
QY 1793 TGATGTGGGGGGGATGCTGCTCATGACCTGTGCATCTGTGTGGAGCTGTGG 1852
DB 63 TGATGTGGGGGGGATGCTGCTCATGACCTGTGTGTCTGTGTGTGTGTGTGTGTGTG 122
QY 1853 ACCCCCTGCGAGAGAGTAGAGAGAGTACATGAGAGCCGAGCCGAGCCGCGGACA 1912
DB 123 ACCCCCTGCGAGAGAGTAGAGAGAGTACATGAGAGCCGAGCCGAGCGGATG 182
QY 1913 TCTCATTCGCGCCATTTGCTGGAAGACTGCGAAACACCCACATGACATCTGGCTTGCA 1972
DB 183 TCTCATTCGCGCCATTTGCTGGAAGACTGCGAAACACCCACATGACATCTGGCTTGCA 242
QY 1973 TTGTCTACGCTTACAGAGGGGCTCTCATGCTATTCGCTGTCTTCTTGGCATGGGAAACC 2032
DB 243 TGTCTATGCTTACAGAGGACTTCTCATGTGTGCTGTGTGTGTGTGTGTGTGTGTG 302
QY 2033 GCAA 2036
DB 303 GCAA 306

RESULT 6
X51891
ID X51891 standard; DNA; 361 BP.
AC X51891:
DE 22-JUN-1999 (first entry)
DE Human secreted protein 5' EST SEQ ID NO: 105.
DE Human secreted protein; EST: expressed sequence tag; diagnosis;
KW Human; secreted protein; EST: expressed sequence tag; signal peptide;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokine; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
OS Homo sapiens.
PN WO9906552-A2.
PD 11-FEB-1999.
PE 31-JUL-1998; 1B1236.
PR 01-AUG-1997; US-905223.
PA (GIST) GENSET.
PI Duclert A, Dumas M, Edwards J, Lacroix B;
DR P-PDB; Y13091.
PT New isolated brain-derived nucleic acids - used to develop products
PT which may have cytokine, immune, regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
PS Claim 1; Page 253; 577pp; English.
CC X51891 to X52019 represent 5' expressed sequence tags (ESTs) for human
CC secreted proteins, and encode the proteins given in Y12967 to Y13219,
CC respectively. The proteins given represent the signal peptide and an
CC N-terminal fragment of a secreted protein. The nucleic acid sequences
CC can be used for producing secreted human gene products. They can also
CC be used to develop products for diagnosis and therapy. The proteins
CC obtained may have cytokine activity, cell proliferation/differentiation
CC activity, haematopoiesis regulating activity, tissue growth regulating
CC activity, reproductive hormone regulating activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, tumour inhibition activity
CC or other activities. The products can be used in forensic, gene therapy
CC and chromosome mapping procedures. The sequences can also be used for
CC obtaining corresponding promoter sequences. The nucleic acids encoding
CC the signal peptide can be used for directing extracellular secretion of

CC a polypeptide or the insertion of a polypeptide into a membrane, or
CC importing a polypeptide into a cell.
SQ Sequence 361 BP; 86 A; 89 C; 94 G; 92 T;

Query Match 5.1%; Score 143.4; DB 1; Length 361;
Best Local Similarity 80.4%; Pred. No. 5.4e-20;
Matches 168; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 287 ACTTCTGGAGCTGCGACTGCTATGACACCGAGTGTGACCAATGCAAGAGACTGAAGCCT 346
DB 153 AGTCATCTATTGTTGGAGCGCAATCATGTCAGTGCAGACACGCAAAAGGTTGAAGCCT 212
QY 347 TCTATGACCAATAAGATGATGGCCGCAACCATTTGATGGTTTGAAGCGCTGTGCGT 406
DB 213 TCTATGATGATATAAATATAGCGGCTTACCACTGATGTGTTGAGAGCGCTGTGCAT 272
QY 407 CMTGACATCTATTATCGCGAGATCCTTCGAAGGCTGGAATCTGGTGTGACGTTTCTTCG 466
DB 273 CCGTACATCATCATATTCAGAGTCCCTCCAAAGGCTGGAATCTGTGTGACGTTTCTTCG 332
QY 467 CCGCAACACGCGCTGTCTTGGGATAG 495
DB 333 CTGCAACACGCGCTGTCTTAGCCGATAG 361

RESULT 7
027091/c
ID 027091 standard; DNA; 1028 BP.
AC 027091:
DE 25-JAN-1993 (first entry)
DE XTR26 probe.
KW Fragile X locus; replacement therapy; (CCG)n repeat; Xq27.3;
KW Cpg island; ss.
OS Homo sapiens.
PN WO9212262-A.
PD 23-JUL-1992.
PE 03-JAN-1992; U00020.
PR 04-JAN-1991; US-638518.
PR 20-MAR-1991; US-672232.
PR 06-DEC-1991; US-802650.
PA (ADEL-) ADELAIDE MEDICAL CENT WOMEN & CHILDREN.
PI (UNIW) UNIV WASHINGTON.
PI Nagaraia R, Richards R, Schlessinger D, Sutherland GR;
DR WPI; 92-268680/32.
PT DNA spanning the Fragile X site on the human X chromosome - for
PT diagnosis and treatment of associated mental retardation
PS Claim 8; Page 23; 47pp; English.
CC This sequence or an effective fragment of it, may be used as a probe
CC for the human Fragile X locus. This probe crosses the fragile site
CC and can be seen to be useful in replacement therapy. Affected
CC individuals appear to have an amplification of a (CCG)n repeat
CC sequence at the fragile site which gives a band of a different size
CC than a normal individual when Southern blots are probed with this
CC probe. The fragile site occurs at the Xq27.3 locus on the X-
CC chromosome. It is in the immediate proximity of a Cpg island and is
CC therefore thought to interfere with the expression of a gene or the
CC function of its' product, this is thought to be the molecular
CC basis of the disease.
SQ Sequence 1028 BP; 128 A; 327 C; 412 G; 161 T;

Query Match 2.2%; Score 63.4; DB 1; Length 1028;
Best Local Similarity 63.4%; Pred. No. 0.00039;
Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 3 GGCTTCCCGCCGAGCTCGGGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 62
DB 463 GCG 404
QY 63 CCTCTGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
DB 403 GCG 344

Qy	123	GAGCGGGGCCCCCCCCCGCCGCCACGAC	155
Dn	343	CCCCCGCCCGCTCAGAGGCGGCCCTCCACC	311
Db			
RESULT	8		
Q51731/c			
ID	051731 standard; DNA: 10596 BP.		
AC	051731;		
Dm	31-MAY-1994 (first entry)		
DE	Plasmid pClISEBON for subcloning huncF variants.		
KM	Hepatocyte Growth Factor; HGF variant; mutant; in vitro mutagenesis;		
KW	proteolysis resistant; liver; malignancy; CMV-driven;		
OS	Cytomegalovirus; episomal expression plasmid; ss.		
Synthetic.			
FH Key	Location/Qualifiers		
FT enhancer	1..611		
FT FT	/tag= a		
FT FT	/note= "CMV enhancer/promoter"		
FT promoter	758..775		
FT FT	/tag= b		
FT FT	/label= SP6_promoter		
FT misc_feature	845..849		
FT FT	/tag= c		
FT FT	/note= "SP6 RNA start"		
FT misc_feature	902..966		
FT FT	/tag= d		
FT FT	/function= cloning_linker		
FT poly_a_signal	967..1107		
FT FT	/tag= e		
FT FT	/note= "SV40 poly A"		
FT misc_feature	1108..1531		
FT FT	/tag= f		
FT FT	/function= SV40_Origin		
FT misc_feature	1580..4189		
FT FT	/tag= g		
FT FT	/label= EBNA-1		
FT misc_feature	4190..6374		
FT FT	/tag= h		
FT repeat_region	/function= orip		
FT FT	4295..4887		
FT FT	/tag= i		
FT FT	/note= "family of repeats"		
FT misc_structure	5866..5978		
FT FT	/tag= j		
FT FT	/note= "dyad region"		
FT terminator	6375..6457		
FT FT	/tag= k		
FT cds	/label= HSV_TK Terminator_3'-end		
FT FT	6975..7975		
FT FT	/tag= l		
FT phenotypic_neomycin_resistance			
FT FT	/note= "Trs neomycin phosphotransferase gene"		
FT FT	7975..8112		
FT promoter	/tag= m		
FT FT	/label= TK_promoter		
FT misc_feature	8114..8594		
FT FT	/tag= n		
FT FT	/function= M13_ori		
FT misc_rna	8595..10414		
FT FT	/tag= o		
FT FT	/label= delta_2a		
PN NO9323541-A.			
PD 25-NOV-1993.			
PF 17-MAY-1993.	U04648.		
PR 18-MAY-1992.	US-884811.		
PR 18-MAY-1992.	US-885971.		
(GETH) GENENTECH INC.			
PI Godowski PJ. LOKKER NA.	Mark MR:		
Pt WPI: 93-386573/48.			
Pr Hepatocyte growth factor variants - are resistant to proteolytic cleavage into its two-chain form, used to treat malignancies			

PT	associated with HGF receptor
PS	Example 1; Fig 6; 87pp; English.
CC	Plasmid pCISEBON (a PKR5 derivative) is an episomal CMV driven
CC	expression plasmid. hHGF variants w/ enhanced receptor binding
CC	actively were produced by site-directed mutagenesis. Stable
CC	populations of preferred HGF variants were obtained by transfecting
CC	human embryonic kidney 293 cells and then these were subcloned in
CC	pCISEBON. See R52940-R52949 for examples of pref. HGF variants.
SQ	Sequence 10596 BP; 2625 A; 2571 C; 3024 G; 2376 T;

Query Match	2.1%;	Score 59.8;	DB 1;	Length 10596;	
Best Local Similarity	50.5%;	Pred. No. 0.003;	Mismatches 142;	Indels 0;	Gaps 0
Matches 145;	Conservative 0;	Mismatches 142;	Indels 0;	Gaps 0	
QY	20	CCGAGGACGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGCCTTC	79		
Db	2614	CCCCCTGCTCTCTGCGCCCTTCTCCCTCTGCGCCCTCTCTCTCTCTCTCTCTCT	2555		
OY	80	TGCTGTGGCTGCTGT	139		
Db	2554	TCTTGCCCT	2435		
OY	140	GCG	199		
Db	2494	TGCTCTGCGCCCT	2435		
OY	200	TGGCGAAGGAGAGATGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	259		
Db	2434	TGCCCCCT	2375		
OY	260	TCCGCAAGAGTACTCTCTGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	306		
Db	2374	TCTGCGCCCT	2328		

RESULT	9
T40348/c	
ID	T40348 standard; DNA; 10596 BP.
AC	T40348;
DT	09-DEC-1996 (first entry)
DE	Human pCISEBON for expression of hepatocyte growth factor.
KW	Human; hepatocyte growth factor; HGF; huHGF; serum; proteolytic cleavage;
KW	pro-hormone; beta subunit; alpha subunit; kringle domain; prothrombin;
KW	plasmaogen; catalytic domain; serine protease; HGF variant;
KW	HGF receptor; malignancy; chronic HGF receptor activation; ss.
OS	Synthetic.
PN	US5347836-A.
PD	20-AUG-1996.
PF	18-MAY-1992; 884811.
PR	18-MAY-1992; US-885971.
PR	18-MAY-1992; US-884811.
PA	13-JUL-1993; US-087783.
PA	(GENTH) GENENTECH INC.
PI	Godowski PJ, Lokker NA, Mark MR; WPL; 96-392634/39.
PT	New hepatocyte growth factor variants - are resistant to in vivo
PT	proteolytic cleavage into a 2-chain form, useful as HGF antagonists
PS	Example 1; Fig 6; 39pp; English.
CC	This sequence represents the episomal CMV driven expression plasmid
CC	pCISEBON which was used in the expression of variant human hepatocyte
CC	growth factor (HGF). HGF is isolated from human serum and is a
CC	disulphide linked heterodimer derived by proteolytic cleavage of the
CC	pro-hormone between residues 494 and 495. This generates a molecule
CC	composed of an alpha subunit of 440 amino acids (mol. wt. 69 kD) and
CC	a beta subunit of 234 amino acids (mol. wt. 34 kD). The alpha and beta
CC	subunits are encoded by a single open reading frame. The alpha subunit
CC	contains four kringle domains based on their homology to kringle-like
CC	domains in other proteins, e.g. prothrombin, plasminogen. The beta
CC	subunit shows high homology to the catalytic domain of serine proteases.
CC	However two of the three residues which form the catalytic triad of
CC	serine proteases are not conserved in HGF. Therefore, the precise
CC	function of the beta chain remains unknown. The invention includes HGF

Db 81 GCTGCTGCCCCGCGGCCCCGCGGAGCGGGAGCCCGCCCTTCCCCGCGCTCGCCGCGC 140
QY 147 GCCCAGCAGCCCGCGCGCTCTCCATCATGGCCCTCATGCCGC 187
Db 141 GCTGAGCCTGCGCGCCCTCGCGGAGCGGGGCTGGAGCTGC 181

Search completed: March 16, 2000, 17:43:01
Job time: 3925 sec

Page 1

Db 2554 TCGGCCCCCTGCCCCCTCCCTGCTCCCTGCCCCCTCCTCC 2495

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 16:24:44 ; Search time 2783.46 Seconds
(without alignments)
-3538.772 Million cell updates/sec

Title: US-09-211-755-1
Perfect score: 3244
Sequence: 1 TGACCTCGGGCAGGTCCTG.....CTTGCAAAAAAAAAAAAAA 3244

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl.*

Word size : 0
Number of hits that pass the threshold : 1642386

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pr1.*
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- 12: gb_ro.*
- 13: gb_sts.*
- 14: gb_sy.*
- 15: gb_un.*
- 16: gb_vl.*
- 17: em_fun.*
- 18: em_hum1.*
- 19: em_hum2.*
- 20: em_in.*
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- 28: em_sts.*
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- 32: gb_htg1.*
- 33: gb_htg2.*
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- 35: gb_in2.*
- 36: em_ba1.*
- 37: em_ba2.*
- 38: em_hum3.*
- 39: em_hum4.*
- 40: gb_pr4.*
- 41: gb_htg3.*
- 42: gb_htg4.*
- 43: gb_htg5.*
- 44: gb_htg6.*
- 45: gb_htg7.*
- 46: em_htg1.*
- 47: em_htg2.*
- 48: em_htg3.*
- 49: em_hum5.*

50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2964.8	91.4	5786	11	AF056085	Homo sapi
2	2961.6	91.3	3155	40	AF099033	AF099033 Homo sapi
3	2928.6	90.3	3240	40	AF095784	AF095784 Homo sapi
4	2752.2	84.8	3075	40	AF069755	AF069755 Homo sapi
5	2664	82.1	2826	40	AF074483	AF074483 Homo sapi
6	2659.2	82.0	2826	10	HS012188	AF012188 Homo sapi
7	2308.2	71.2	3288	12	AFI09405	AFI09405 Rattus no
8	2308.2	71.2	5614	12	RN0011318	AF011318 Rattus no
9	2304.2	71.0	5459	12	AF058795	AF058795 Rattus no
10	2218.2	68.4	2823	12	AF074482	AF074482 Rattus no
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12	649	20.0	740	11	AF095724	AF095724 Homo sapi
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16	317.2	9.8	2928	9	HS025029	AJ225029 Homo sapi
17	317.2	9.8	2535	10	HS012186	AJ012186 Homo sapi
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ALIGNMENTS

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LOCUS AF056085 5786 bp mRNA PRI 08-OCT-1998
DEFINITION Homo sapiens GABA-B receptor mRNA, complete cds.
ACCESSION AF056085
VERSION AF056085.1 GI:3719225
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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REFERENCE 1 (bases 1 to 5786)


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RESULT 2
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LOCUS Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2)
DEFINITION mRNA, complete cds.
ACCESSION AF099033
VERSION AF099033.1 GI:5639666
KEYWORDS human.
SOURCE Homo sapiens
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3155)
AUTHORS Martin,S.C., Russek,S.J. and Farb,D.H.
TITLE Molecular identification of the human GABABR2: cell surface
expression and coupling to adenylyl cyclase in the absence of
GABABR1
JOURNAL Mol. Cell. Neurosci. 13 (3), 180-191 (1999)
MEDLINE 99263199
REFERENCE 2 (bases 1 to 3155)
AUTHORS Martin,S.C., Russek,S.J. and Farb,D.H.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1998) Laboratory of Molecular Neurobiology,
Department of Pharmacology, Boston University School of Medicine,
715 Albany Street, L606, Boston, MA 02118-2394, USA

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Matches 2964; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DEFINITION AF095784
ACCESSION AF095784
VERSION AF095784.1 GI:4836217
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3240)
AUTHORS Liu,M., Parker,R., McCreas,K., Watson,J., Baker,E., Sutherland,G.
and Herzog,H.
TITLE Cloning and characterization of a novel human GABA-B receptor
subtype with high affinity for GABA and low affinity for baclofen
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3240)
AUTHORS Liu,M., Parker,R., McCreas,K., Watson,J., Baker,E., Sutherland,G.
and Herzog,H.
TITLE Direct Submission
JOURNAL Submitted (15-Nov-1998) Neurobiology Program, Garvan Institute of
Medical Research, 384 Victoria St, Sydney, NSW 2010, Australia
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VERSION	AF069755.1	GI:4091932	
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Ng,G.T.K., McDonald,T., Bonner,T., Ribby,M., Heavens,R., Whiting,P., Chateaufort,A., Coulombe,N., Kargmen,S., Caskey,T., Evans,J., O'Neill,G.P. and Liu,Q.			
Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9			
Genomics 56 (3), 288-295 (1999)			
2 (bases 1 to 3075)			
McDonald,T. and Liu,Q.			
Direct Submission			
Submitted (03-JUN-1998) Human Genetics, Merck Research Labs, West Point, PA 19486, USA			
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LOCUS Homo sapiens GABA-B receptor 2 mRNA, complete cds.
DEFINITION AF074483
ACCESSION AF074483.1 GI:4107511
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2826)
AUTHORS Borowsky,B., Laz,T. and Gerald,C.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Department of Molecular Biology, Synaptic
Pharmaceutical Corporation, 215 College Road, Paramus, NJ 07652,
USA
2 (bases 1 to 2826)
AUTHORS Borowsky,B., Laz,T. and Gerald,C.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1999) Department of Molecular Biology, Synaptic
Pharmaceutical Corporation, 215 College Road, Paramus, NJ 07652,
USA
REMARK
COMMENT Sequence update by submitter
FEATURES On Jan 7, 1999 this sequence version replaced gi:4038343.
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ACCESSION AJ012188
VERSION AJ012188.1 GI:3776097
KEYWORDS GABAB receptor; gabab-R2 gene; subunit 2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE White,J.H., Wise,A., Main,M.J., Green,A., Fraser,N.J., Disney,G.H.,
Barnes,A.A., Emsom,P., Foord,S.M. and Marshall,F.H.
Heterodimerization is required for the formation of a functional
GABA(B) receptor
Nature 396 (6712), 679-682 (1998)
JOURNAL MEDLINE 99087321
REFERENCE 2 (bases 1 to 2826)
AUTHORS Fraser,N.J.
TITLE Direct Submission
SUBMITTED 16-OCT-1998 Fraser N.J., Receptor Systems, Cellular
Sciences, GlaxoWellcome, Medicines Research Centre, Gunnel's Wood
Road, Stevenage, Herts. SG1 2NY, U.K
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Qy	697	TGGAAGCGCGTGGGAGCGCTGACGAGAGAGTTCAGAGGTTCTGTAGGTCCGGAATGAC	756
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Qy	757	CTGACTGGAGTTGTGTATGCGAGAGCAATTGAGATTTCCAGACACGAGAGCTTCTCCAC	816
Db	757	CTGACTGGGGTTCTGTATGCGGGAAGATATGAGATCTCAGACACAGAGAGCTTCTCCAAT	816
Qy	817	GATCCCTGATACAGTGTAAAAAGCTGAAGGGAATGATGTGCGGATATCTTTGGCCAG	876
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Qy	877	TTTGACCAAGATATGGGACCAAAAGTGTGTTGTGTGATCGAGGAGAAATCATATAGT	936
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Db	997	GTTGGAGGCAATCTCTCACGCTGCTGCGAGAGCCCTCTCGGCTCCATGGAAGGTTAC	1056
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Db	1057	ATTGGAGTGGATTTGAGAGCCCTGAGCTCCAACATCAAGACCATTCTCGAGAAAGCT	1116
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Qy	1177	CACGGGTACGCTACGATGAGCATCTGGGTATCTGCCAAGACACTGCAAGGGCCATGGAG	1236
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Db	2497		
Qy	2497	AACCAACCCCTTCGAAATGAAGATCACAGACTGTGCAAAAAGACTTTGGAAGAGTACCATG	2556
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LOCUS	RNM011318		
DEFINITION	Rattus norvegicus mRNA for GABA-B R2 receptor.		18-DEC-1998
ACCESSION	AF011318		
VERSION	AF011318.1 GI:4029344		
KEYWORDS	gaba-B R2 gene; GABA-B R2 receptor.		
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
REFERENCE	1. Eukariyota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.		
AUTHORS	Kaupmann,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-SEP-1998) Kaupmann K., TA Nervous System, Novartis		
REFERENCE	Pharma AG, K-125.6.20, CH-4002 Basel, SWITZERLAND		
	2 (bases 1 to 5614)		

AUTHORS	TITLE	JOURNAL MEDLINE FEATURES
Kaupmann, K., Maltischek, B., Schuler, V., Held, J., Froestl, W., Beck, P., Mosbacher, U., Bischoff, S., Kulik, A., Shigemoto, R., Karschin, A. and Bettler, B.	GABA(B)-receptor subtypes assemble into functional heteromeric complexes	Nature 396 (6712), 683-687 (1998) 99087332
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BASE COUNT	1374 a 1664 c 1436 g 1140 t	
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Query Match	71.2%; Score 2308.2; DB 12; Length 5614;	
Best Local Similarity	87.8%; Pred. No. 0;	
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DEFINITION	Rattus norvegicus GABA-B receptor gb2 mRNA, complete cds.			15-Oct-1998
ACCESSION	AF058795			
VERSION	AF058795.1	GI:3746525		
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ORGANISM	Rattus norvegicus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
TITLE	1 (bases 1 to 5459)			
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.			
REFERENCE	gb2, A second GABA-B receptor			
AUTHORS	Unpublished			
TITLE	2 (bases 1 to 5459)			
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (09-APR-1998) section on Genetics, NIMH, Bldg. 36, Km.			
JOURNAL	3D06, MSC 4094, Bethesda, MD 20892-4094, USA			
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Query Match	Best Local Similarity	Matches 2603	Conservative	2	Mismatch	335	Indels	29	Gaps	7
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310	CCGCTCTCCATCATATGGCGCTCATGCGCGCTCA	CCAAAGGAGTGGCGCAAGGCGCAGCATGGG	369							
337	CGCGGTGTGCTCCCCCGCGTGAATGGCCATGAG	CAGATCCGCAACGATCCTCTG	396							
370	CGCGCGTGTCTCCCCCGCGTGAATGGCCATGAG	CAGATCCGCAACGATCCTCTG	429							
397	CGCGCGTGTCTCCCCCGCGTGAATGGCCATGAG	CAGATCCGCAACGATCCTCTG	456							
430	CGCGCGTGTCTCCCCCGCGTGAATGGCCATGAG	CAGATCCGCAACGATCCTCTG	489							
457	AAAGCCTTCTACGATGCGATAAATACGGCGCGA	ACCCTGATGATGTGTGGAGCGTC	516							
490	AAAGCCTTCTACGATGCGATAAATACGGCGCGA	ACCCTGATGATGTGTGGAGCGTC	549							
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577	TCTTTTGTGTGAACACGCGCTGTCTTACGCGAT	TAAGAAAAATACCTTATTTCTTCCG	636							
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637	ACCGTCCATCAGACATATGGCGTGAATCCAGCAT	TTTGAAGTTGCTCCAGACTACG	696							
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AF074482
AF074482.1 GI:4107510
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2823)
AUTHORS Jones, K.A., Borowsky, B., Tamm, J.A., Craig, D.A., Durkin, M.M.,
Dai, M., Iao, W.-J., Johnson, M., Gunwaldsen, C., Huang, D.-Y., Tang, C.,
Shen, Q., Salton, J.A., Morse, K., Laz, T., Smith, K.E., Nagarathnam, D.,
Noble, S.A., Branchek, T.A. and Gerald, C.
GABA(B) receptors function as a heteromeric assembly of the
subunits GABA(B)R1 and GABA(B)R2
JOURNAL Nature 396 (6712), 674-679 (1998)
MEDLINE 99087320
REFERENCE 2 (bases 1 to 2823)
AUTHORS Borowsky, B., Laz, T. and Gerald, C.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Department of Molecular Biology, Synaptic
Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,
USA
REFERENCE 3 (bases 1 to 2823)
AUTHORS Borowsky, B., Laz, T. and Gerald, C.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1999) Department of Molecular Biology, Synaptic
Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,
USA
REMARK
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FEATURES On Jan 7, 1999 this sequence version replaced gi:4038341.
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AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 743)		
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.		
REFERENCE	9b2, a second GABA-B receptor		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 743)		
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (27-MAR-1998) Section on Genetics, National Institute of		
TITLE	Mental Health, Bldg 36, Rm 3D06, MSC 4094, Bethesda, MD 20892-4090,		
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Query Match 20.2%; Score 655; DB 11; Length 743;
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 DB 703 CGGGGACAGGGGAGACTGGCACTGACCTGACCTTATT 743

RESULT 12
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 LOCUS Homo sapiens GABA-B receptor splice variant 2 mRNA, partial cds.
 DEFINITION AF095724
 ACCESSION AF095724
 VERSION AF095724.1 GI:3719473

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

AUTHORS

Clark, J.C., Lam, A., and Bonner, T.I.

1 (bases 1 to 740)

gb2, a second GABA-B receptor

Unpublished

REFERENCE

AUTHORS

Clark, J.C., Lam, A., and Bonner, T.I.

2 (bases 1 to 740)

Direct Submission

Submitted (27-MAR-1998) Section on Genetics, National Institute of

Mental Health, Bldg 36, Rm 3D06, MSC 4094, Bethesda, MD 20892-4090,

USA

FEATURES

source

Location/Qualifiers

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			Gaps	0

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 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the places
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* gap of unknown length
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mRNA, complete cds.
ACCESSION
AF145639
VERSION
AF145639.1 GI:5052567
KEYWORDS
fruit fly.
SOURCE
FLI_CDNA.
ORGANISM
Drosophila melanogaster
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
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Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Friese,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Pacleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Svirskaas,R.R., Weinburg,T. and Celniker,S.E.
Full length Drosophila melanogaster cDNA sequence
Unpublished
2 (bases 1 to 3989)
Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Friese,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Pacleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Svirskaas,R.R., Weinburg,T. and Celniker,S.E.
Direct Submission
Submitted (23-APR-1999) Berkeley Drosophila Genome Project,
University of California Berkeley, Berkeley, CA 94720, USA
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
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FEATURES
source
gene
CDS

Tue Mar 21 10:26:18 2000

us-09-211-755-1.rge

Page 24

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Job time: 3696 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 10:54:00 ; Search time 76.48 Seconds

(without alignments)
5078.184 Million cell updates/sec

Title: US-09-211-755-1

Perfect score: 3244

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Searched: 214294 segs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	45.4	1.4	2176	7	5320958-1	Patent No. 5320958
3	43.8	1.4	4095	6	PCT-US91-09422-18	Sequence 18, Appl
4	43.8	1.4	2426	6	PCT-US91-09422-20	Sequence 20, Appl
5	41.8	1.3	1312	1	US-08-205-506A-1	Sequence 1, Appl
6	41.8	1.3	1312	6	PCT-US94-02389-1	Sequence 1, Appl
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8	41.6	1.3	2823	1	US-08-398-008A-1	Sequence 1, Appl
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44	38.2	1.2	2338	2	US-08-455-543A-31	Sequence 31, Appl
45	38.2	1.2	5904	3	US-08-193-078B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1\nUS-08-232-463-14/c\n; Sequence 14, Application US/08232463\n; Patent No. 5670367\n; GENERAL INFORMATION:\n; APPLICANT: DORNER, F.\n; APPLICANT: SCHEFFLINGER, F.\n; APPLICANT: FALKNER, F. G.\n; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS\n; NUMBER OF SEQUENCES: 52\n; CORRESPONDENCE ADDRESS:\n; ADDRESSEE: Foley & Lardner\n; STREET: 1800 Diagonal Road, Suite 500\n; CITY: Alexandria\n; STATE: VA\n; COUNTRY: USA\n; ZIP: 22313-0299\n; COMPUTER READABLE FORM:\n; MEDIUM TYPE: Floppy disk\n; COMPUTER: IBM PC compatible\n; OPERATING SYSTEM: PC-DOS/MS-DOS\n; SOFTWARE: PatentIn Release #1.0, Version #1.25\n; CURRENT APPLICATION DATA:\n; APPLICATION NUMBER: US/08/232,463\n; FILING DATE:\n; CLASSIFICATION: 435\n; PRIOR APPLICATION DATA:\n; APPLICATION NUMBER: US/07/935,313\n; FILING DATE:\n; APPLICATION NUMBER: EP 91 114 300.6\n; FILING DATE: 26-AUG-1991\n; ATTORNEY/AGENT INFORMATION:\n; NAME: BENT, Stephen A.\n; REGISTRATION NUMBER: 29,768\n; REFERENCE/DOCKET NUMBER: 30472/114 IMMU\n; TELECOMMUNICATION INFORMATION:\n; TELEPHONE: (703)836-9300\n; TELEFAX: (703)683-4109\n; TELEX: 899149\n; INFORMATION FOR SEQ ID NO: 14:\n; SEQUENCE CHARACTERISTICS:\n; LENGTH: 7218 base pairs\n; TYPE: nucleic acid\n; STRANDEDNESS: single\n; TOPOLOGY: linear\n; IMMEDIATE SOURCE:\n; CLONE: PTZspt-Fls\n; US-08-232-463-14

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:
: APPLICANT: INOYE, SUNIKO; HSU, MEI-YIN; EAGLE, SUSAN;
: INOYE, MASAYORI
:
: TITLE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASE
:
: NUMBER OF SEQUENCES: 24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/315,316
: FILING DATE: 24-FEB-1989
: SEQ ID NO:1
: LENGTH: 2176
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QY	329	GCATCGGGGGCGGTGTCCTCCCGCCGCGGAATGAGCCATGAGACAAATCCGGAAGAG	388			
Db						
Db	1070	accgccttcgacgagctcggaactcggcgagggcgcgctcgccaagcgctggggctgacacgtgt	1129			
QY	389	CACTCTCGCGCCCCCTACTCTCTGACC	415			
Db						
Db	1130	ccaagctcgctcgtgttcggttccac	1156			

RESULT 3

```

PCT-US91-09422-18
; Sequence 18, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Hounamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4095 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: SM30
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 463..3198
PCT-US91-09422-18

```

	Query Match	1.4%:	Score 43.8:	DB 6:	Length 4095:
	Best Local Similarity	49.4%:	Pred. No. 0.11:		
	Matches 114:	Conservative	0:	Mismatches 117:	Indels 0:
				Gaps	0:
QY	497	TGATGTTGTTGGAGCGCTCTCCATCCGCACATCATCATTTGAGAGTCCCTCCAG	556		
Db	914	TGGGTGTCATGGAGTTCCGGGACATCGTCTGCATCATGATGGCCACATCTCTCCGC	973		
QY	557	GCATGATCTGATGCACTTTCTTTTGGTGCACACGCTGTTCTTAGCCGATAGAGAAA	616		
Db	974	TCTTCAAGATCCCTAGATCAACATATGCTTCCACAGGCCCTGTACTGATGACAAACGCC	1033		
QY	617	AATACCCATTAATCTTTGGGACCGCCCATAGACATGGGGATATCCAGGCATTTCTGA	676		
Db	1034	GCATATGACTTTCTTCCGGGGTGGTCCCTTAGACAAATATCCAGGCCCCAGGCCATGGTGG	1093		
QY	677	AGTTGCTCAGACATCAAGATGGAAGCGGTGGGACGCTGACGCAAGAGC	727		

677 AGTGGCTAAGCACTACCACTGGAAAGCGGTGGGCACGCTGACCGCAAGACG 727

Db 1094 ATATTGTCGACGCCCTCAGAGTGAACATATGTCTCACACTGGCCTCAGAGG 1144

RESULT 4

PCT-US91-09422-20

Sequence 20, Application PC/TUS9109422

GENERAL INFORMATION:

APPLICANT: Mulvihill, Eileen R.

APPLICANT: Hagen, Frederick S.

APPLICANT: Houmed, Khaled M.

APPLICANT: Almers, Wolfhard

TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend

STREET: One Market Plaza, Stewart Street Tower

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/09422

FILING DATE: 19911212

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/672,007

FILING DATE: 18-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/648,481

FILING DATE: 30-JAN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/626,806

FILING DATE: 12-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 13952-6PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 2426 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: SR13

PCT-US91-09422-20

Query Match 1.4%; Score 43.8; DB 6; Length 2426;

Best Local Similarity 49.4%; Pred. No. 0.083;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 677 AGTGTCTCAGACACTACAGTGAAGCGCGTGGACCGCTGACGACAGC 727

Db 344 ATATTGTCGACGCCCTCAGAGTGAACATATGTCTCACACTGGCCTCAGAGG 394

RESULT 5

US-08-205-506A-1

Sequence 1, Application US/08205506A

Patent No. 5545563

GENERAL INFORMATION:

APPLICANT: Darlington, Gretchen J.

APPLICANT: Wilson, Deborah R.

APPLICANT: Wilde, Margaret

TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR

NUMBER OF SEQUENCES: ITS EXPRESSION

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 801 Pennsylvania Avenue, NW

CITY: Washington, D.C.

STATE:

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/205,506A

FILING DATE: March 4, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Davis, Peter J.

REGISTRATION NUMBER: 36,119

REFERENCE/DOCKET NUMBER: 311,027

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 662-4643

TELEFAX: (202) 662-4643

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1312 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: C/EBP

US-08-205-506A-1

Query Match 1.3%; Score 41.8; DB 1; Length 1312;

Best Local Similarity 54.1%; Pred. No. 0.2; DB 1; Length 1312;

Matches 85; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2818 GCGTACCTCCATCCATCGAGGCGTGAAGCGCAGCTGTGACGCCCTGCGTCAAGCC 2877

Db 797 GCGAGACACACATGACGCTGCGAGCGGACCGACCGACGCGCGCGCGCGCGCA 856

QY 2878 ACCGCCAGGCCCCGACAGAGATGTCGACCGCTCTTCCAGTATGCTCGGGCCTG 2937

Db 857 GCGCGACCCCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCA 916

QY 2938 TAAGGTGGAGGCGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2974

Db 917 AGGGGCTGGGCGAG 953

```
RESULT 6
PCT-US94-02389-1
; Sequence 1, Application PC/TUS9402389
; GENERAL INFORMATION:
; APPLICANT: Darlington, Gretchen J.
; APPLICANT: Wilson, Deborah R.
; APPLICANT: Wilde, Margaret
; TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR ITS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02389
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I.
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 225-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: C/EBP
; PCT-US94-02389-1

Query Match 1.3%; Score 41.8; DB 6; Length 1312;
Best Local Similarity 54.1%; Pred. No. 0.2;
Matches 85; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2818 GCCTACCTCCATCATGAGAGGCTGACGCCACTGTGTCAGCCCTGCGTCAGCCCC 2877
DB 797 GCCAGACACCATGACCTGACGACCCGCGGTGACCCGCGCCGCGCCGCGCTGACCA 856
QY 2878 ACCGCCAGCCCCCGCCACAGACATGTGACACCCCTCCGAGTCATGTCGCGGCGCTG 2937
DB 857 GCCCGACACCGCGCGCGCGCTGCTGCGCGCGCGCTTCGCGGCGCTTCGAGCGGCTCA 916
QY 2938 TAAGGTTGAGAGCCTGGGCGCGCGGCGCTCCCGCGTG 2974
DB 917 AGGGGCTGGGCGCGCGACCCCGGACCTCGGCGGAG 953

RESULT 7
US-07-945-283-1/c
; Sequence 1, Application US/07945283
; Patent No. 5352596
; GENERAL INFORMATION:
; APPLICANT: Cheung, Andrew K.
; APPLICANT: Wesley, Ronald D.
```

```
; TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
; TITLE OF INVENTION: Involving The EP0 and LIT Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtiss P. Ribando
; STREET: 1815 No. 5352596th University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: USA
; ZIP: 61604
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,283
; FILING DATE: 19920911
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P.
; REGISTRATION NUMBER: 27976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309-685-4011 ext. 513
; TELEFAX: 309-685-4128
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8438 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 622..6495
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1099, "g")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1267, "t")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1381, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1566, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(7010, "g")
; US-07-945-283-1

Query Match 1.3%; Score 41.6; DB 1; Length 8438;
Best Local Similarity 48.1%; Pred. No. 0.54;
Matches 148; Conservative 0; Mismatches 159; Indels 1; Gaps 1;

QY 132 CCGGTCCAGGCTGGGCGGAGTCGAGGCGGAGAGCGCGCTGAGTGCAGAGTCC 191
DB 4305 CCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4246
QY 192 AGAGCCGTGCGCCCGCCAGAACTGCGCTCGCGCCCGGTCAGACCCCGCGCGCATGCCAG 251
DB 4245 AGCCCGGACAGACCAAGTCCGCTCCAGCACCAAGTCCAGCTCCGGACCAAGTCCGGC 4186
QY 252 TTGCCCCGCGGCTGCTGATGAGGCGCGCTCTCATATGAGGCTCATGCGCTACACAA 311
DB 4185 CTCCTCGGCTCTCCGCTAGCGACAGCTCCCGCGCGCGCGCGGAGCCGAGC-CGA 4127
```

QY 312 GGAGTGGCCAAAGGACATCGGGCGGTGTGTCCTCCCGCCTGGAACCTGACATCGA 371
Db 4126 GCGGGCAAGGAAGACCCCGCGCCGCGGGCCCGCGCCCGCGGAGGAGA 4067
QY 372 GCAGATCCGACAGGACTCTGCGCCCTACTCTCCAGCTGGGGCTCTATGACAC 431
Db 4066 CGAGGGGCTCTCGGCTCGCCCTCCGCGGAGCGCCACCGCAGCAGAGA 4007
QY 432 GGAGTGC 439
Db 4006 GGACCGG 3999

RESULT 8

US-08-398-008A-1/c
; Sequence 1, Application US/08398008A
; Patent No. 5655588

GENERAL INFORMATION:

APPLICANT: Kornbluth, Jacki
TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gilbreth & Adler, P.C.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: MACINTOSH IIfx
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,008A
FILING DATE: March 2, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/126,501
FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Adler, Dr. Benjamin Aaron
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5705CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2823 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-398-008A-1

Query Match 1.3%; Score 41.6; DB 1; Length 2823;

Best Local Similarity 44.7%; Pred. No. 0.32;
Matches 161; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 2778 CCAGCGTGGCTGCTCCCTCCAGCTCCCATCTCCACAGGCTACTCCCATCCATCGG 2837
Db 559 CCAGCGACAGCGGACACTCTCCCTCCCGCCCGGCGCCACCGCTCCGCGCTCCT 500
QY 2838 AGCGTGGAGCGACCTGTGTCAGCCCTGGGTGACGCCACCGCGACGCCCGCGACAG 2897
Db 499 CATGTGCAACCGAGCTCCGCCCCCGCGCGCGGCTCCGCTCGGCTGGGCGCG 440

QY 2898 ACATGTGCCACCTCTCTCCGATATGTGTCTGGGCTCTGTAAGGTGGAGGCTGGGC 2957
Db 439 GCTCGCGGGGCAAGCGGCTGTGGCGGGGCTCTGGGCTCCGCGCGGAGGGCGGGCGG 380
QY 2958 CCGGGGCTTCCCGCCGACAGAACCACTGGGCGAGAGGGGTCTCTGCAGAACACTGT 3017
Db 379 GCGGGCGGAGCGGGGCGGGGCTCGGCTCGGCTTGGCCCCGGGGGCGGGCGG 320
QY 3018 CGGCTCTGGCTGGAGAACTGGGACCATGCTGGCTCTCAGAGCACTCGGATGGC 3077
Db 319 GGGCGAGGAGAGAGAGAGCTGTGCAAGTGAAGGGCGCGGCGCGCGCTGCGGC 260
QY 3078 ACTCAGGTGACAGAGCGGGGAGAGGAGACTTGGCACCTGACCTCGAGCTTATTGT 3137
Db 259 ACTTAGGCTCGGGTGGCGCGCATGTAGCATGTGAGCGCGGCACTCGAGTCTTCT 200

RESULT 9

US-08-893-333-1/c
; Sequence 1, Application US/08893333A
; Patent No. 5981705

GENERAL INFORMATION:

APPLICANT: Kornbluth, Jacki
TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated Protein
FILE REFERENCE: D5705CIP/D
CURRENT APPLICATION NUMBER: US/08/893,333A
CURRENT FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 1

LENGTH: 2823

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

LOCATION: 190..1953

OTHER INFORMATION: CDS

US-08-893-333-1

Query Match 1.3%; Score 41.6; DB 4; Length 2823;

Best Local Similarity 44.7%; Pred. No. 0.32;
Matches 161; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 2778 CCAGCGTGGCTGCTCCCTCCAGCTCCCATCTCCACAGGCTACTCCCATCGATCGG 2837
Db 559 CCAGGACAGAGGAGCACTCCACTCTCCCGCGCGGCGCACCGGCTCGCGCTCCT 500
QY 2838 AGCGTGGAGCGGACCTGTGTCAGCCCTTGGCTCAGCCCGCACCGGCGCGACAG 2897
Db 499 CATGTGCAACCGAGCTCCGCCCCCGCGCGCGGCTCCGCTCGGCTGGGCGCG 440
QY 2898 ACATGTGCCACCTCTCTCCGATATGTGTCTGGGCTCTGTAAGGTGGAGGCGCTGGGC 2957
Db 439 GCTCGGGGCGGAGCGGCTGTGGCGGGGCTCTGGGCTCCGCGCGGAGGGCGGGCGG 380
QY 2958 CCGGGGCTTCCCGCCGACAGAACCACTGGGCGAGAGGGGTCTCTGCAGAACACTGT 3017
Db 379 GCGGGCGGAGCGGGGCGGGGCTCGGCTCGGCTTGGCCCCGGGGGCGGGCGG 320
QY 3018 CGGCTCTGGCTGGAGAACTGGGACCATGCTGGCTCTCAGAGCACTCGGATGGC 3077
Db 319 GGGCGAGGAGAGAGAGCTGTGCAAGTGAAGGGCGCGGCGCGCGCTGCGGC 260
QY 3078 ACACAGGTGAGAGAGGCGGAGGAGAGCTTGGCACCTGACCTCGAGCTTATTGT 3137
Db 259 ACTTAGGCTCGGGTGGCGCGCATGTAGCATGTGAGCGCGGCACTCGAGTCTTCT 200

RESULT 10

US-07-884-811-15/c
; Sequence 15, Application US/07884811
; Patent No. 5316921

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.


```
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,087
FILING DATE: 18-May-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ. ID NO: 15:
LENGTH: 10596 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-194-087-15
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```
Query Match          1.3%; Score 40.6; DB 3; Length 10596;
Best Local Similarity 50.2%; Pred. No. 1.1;
Matches 126; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
```

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OY 189 TCCAGAGCCGTGCGCCCAAGAACTGCGGCTCCGCCCGGCAACCCCGCGCCCATGCC 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2464 TCCGTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2405

OY 249 CAGTTGCCCGCGCGCTGTGCTAGCGGCC-6GCTCCATCATGGGCGCTCATGCCGTCA 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2404 CCTCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2345

OY 308 CCAAGAGGTGCGCAAGGCAATCGGCGCGGTGTCTCCCGCGCGTGAAGTGGCA 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2344 TCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2285

OY 368 TCGAGCAGATCCGCAAGAGTACTCTGCGCCCTTCTCTGAGCTGCGGCTCTATG 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2284 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2225

OY 428 ACACGAGTGC 438
    ||| ||| |||
Db 2224 ACCGTGGGTCC 2214
```

```
RESULT 15
US-09-130-114-1
: Sequence 1, Application US/09130114
: Patent No. 5976807
: GENERAL INFORMATION:
: APPLICANT: Horlick, Robert A.
: APPLICANT: Dama, Bassam B.
: APPLICANT: Robbins, Alan K.
: TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
: FILE REFERENCE: 0867/1D903051
: CURRENT APPLICATION NUMBER: US/09/130,114
: NUMBER OF SEQ. ID NOS: 36
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ. ID NO. 1
: LENGTH: 3452
: TYPE: DNA
: ORGANISM: VEBNA
US-09-130-114-1
```

```
Query Match          1.3%; Score 40.6; DB 4; Length 5452;
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Best Local Similarity 50.2%; Pred. No. 0.79;
Matches 126; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

OY 189 TCCAGAGCCGTGCGCCCAAGAACTGCGGCTCCGCCCGGCAACCCCGCGCCCATGCC 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1921 TCCGTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

OY 249 CAGTTGCCCGCGCGCTGTGCTAGCGGCC-6GCTCCATCATGGGCGCTCATGCCGTCA 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1981 CCTCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040

OY 308 CCAAGAGGTGCGCAAGGCAATCGGCGCGGTGTGCTCCCGCGCGTGAAGTGGCA 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2041 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100

OY 368 TCGAGCAGATCCGCAAGAGTACTCTGCGCCCTTCTCTGAGCTGCGGCTCTATG 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2101 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160

OY 428 ACACGAGTGC 438
    ||| ||| |||
Db 2161 accgtggtcc 2171
```

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Search completed: March 16, 2000, 11:12:08
Job time: 1088 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 11:14:53 ; Search time 1755.56 Seconds
(without alignments)
6976.836 Million cell updates/sec

Title: US-09-211-755-1
Perfect score: 3244
Sequence: 1 TGACCTCGGGCAGGCTCCTG.....CTTGCAAAAAAAAAAAAAA 3244

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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2: em_est2:*
3: em_est3:*
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8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
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14: em_est14:*
15: em_est15:*
16: em_est16:*
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33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*

50: gb_est31:*
51: gb_est32:*
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71: gb_est41:*
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77: em_est33:*
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79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
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83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
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88: gb_gss6:*
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96: em_gss9:*
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98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	637.2	19.6	704 63	A1968032 wu12c11.x
C 2	557.4	17.2	560 45	A1341249 qx90d04.x
C 3	410.2	12.6	416 63	A1937563 wp78c11.x
C 4	408.2	12.6	414 47	A1500214 tm94d05.x
C 5	389.8	12.0	397 43	A121d087 ap29g06.x
C 6	368.2	11.4	384 40	A1000006 oc03b08.s
C 7	355.6	11.0	371 22	H14151 ym62d04.r1

c	8	320.4	9.9	326	20	239716	239716 HSC1H042
	9	315	9.7	341	20	243654	243654 HSC1H041
	10	258	8.0	368	20	T07621	T07621 EST05511_Fe
	11	241.8	7.5	283	31	AA324303	AA324303 EST27126
c	12	235	7.2	235	36	AA613872	AA613872 h081f06.s
	13	223.6	6.9	853	87	AQ744524	AQ744524 HS_5508_A
c	14	134	4.1	136	69	AW138313	AW138313 UI-H-B1-
c	15	132.2	4.1	302	27	AA022569	AA022569 z67h11.r
	16	121.4	3.7	544	42	AI134060	AI134060 GH1409.5
	17	103	3.2	450	64	AL119755	AL119755 DKFZP761C
	18	96.8	3.0	307	22	R76139	R76139 y11b07.r1
c	19	94.8	2.9	512	64	AW049355	AW049355 UI-M-B1-
	20	92.2	2.8	404	35	AA567648	AA567648 HL01578.5
	21	91	2.8	393	71	AW158263	AW158263 za3b08.x
	22	83	2.6	459	61	AI042317	AI042317 DKFZP434N
	23	82.6	2.5	900	87	AQ744512	AQ744512 HS_5508_A
	24	82.2	2.5	619	46	AI040922	AI040922 GH24783.5
	25	75	2.3	417	22	R80448	R80448 y193c05.r1
	26	71.2	2.2	599	46	AI030990	AI030990 GH2355.5
	27	67	2.1	268	31	AA333988	AA333988 EST26929
c	28	66.2	2.0	611	26	X90542	X90542 HSGT545_Hum
	29	65.4	2.0	381	43	AI020961	AI020961 qr32c05.x
c	30	65.4	2.0	394	43	AI0203251	AI0203251 qr29609.x
c	31	65.4	2.0	409	49	AI033778	AI033778 tt28d10.x
c	32	65.4	2.0	409	64	AW071653	AW071653 wt94g05.x
c	33	65	2.0	925	79	CNS0091P	AL053013_Drosophila1
c	34	64	2.0	895	79	CNS0071A	AL066286_Drosophila1
c	35	61.2	1.9	540	41	AI063197	AI063197_GH02730.5
c	36	61	1.9	492	26	X90543	X90543_HSGT546_Hum
c	37	58	1.8	1101	79	CNS00FE	AL071370_Drosophila1
c	38	57.6	1.8	925	79	CNS0091P	AL053013_Drosophila1
c	39	56.4	1.7	398	27	AA036134	AA036134_m175a09.r
c	40	54.6	1.7	844	79	CNS0052P	AL056552_Drosophila1
c	41	52.6	1.6	932	79	CNS00720	AL066742_Drosophila1
c	42	52	1.6	479	42	AI108469	AI108469_GH07312.5
c	43	52	1.6	935	79	CNS006XK	AL066051_Drosophila1
c	44	52	1.6	909	79	CNS00JTL	AL076720_Drosophila1
c	45	51.6	1.6	1009	79	CNS010EM	AL098882_Drosophila1

ALIGNMENTS

RESULT 1 AI968032 704 bp mRNA EST 25-AUG-1999
LOCUS AI968032/c wu12c11.x1 NCI_CGAP_G66 Homo sapiens cDNA clone IMAGE:2516756 3'
DEFINITION similar to TR:075975 075975 GABA-B RECEPTOR SPLICED VARIANT 2 ; ,
mRNA sequence.

ACCESSION AI968032
VERSION AI968032.1 GI:5764850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3189191.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:

FEATURES		source		www.bio.liml.gov/bdrip/image/image.html	
Seq primer: -40UP from G1bco		High quality sequence stop: 461.		Location/Qualifiers	
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/clone="IMAGE:2516756"		/clone_lib="NCI_CGAP_G66"		/tissue_type="pooled germ cell tumors"	
/lab_host="DH10B"		/note="Vector: pT73D-Pac (Pharmacia) with a modified		polylinker; Plasmid DNA from the normalized library	
NCI CGAP G64 was prepared, and ss circles were made in		vitro. Following HAP purification, this DNA was used as		tracer in a subtractive hybridization reaction. The driver	
was PCR-amplified cDNAs from a pool of 5,000 clones made		from the same library (clonoids 1257096-1258631,		1469064-1470983, and 1475592-1476743). Subtraction by	
Bento Soares and M. Fatima Bonaldo."		BASE COUNT		124 a 183 c 212 g 182 t 3 others	
ORIGIN		Query Match		19.6%; Score 637.2; DB 63; Length 704;	
Best Local Similarity 96.5%; Pred. No. 3e-139;		Matches 682; Conservative 0; Mismatches 21; Indels 4; Gaps 3;			
QY	2524	GAGCTGGATTAAGACTTGGAGAGGTACACATGACGTGACAGACACCAAGAAAGACC	2553		
DB	704	GAGCTGTAATTAAGACTTGGAGAGGTACACATGACGTGACAGACACCAAGAAAGACC	647		
QY	2584	ACCTCATTAACAGAC	2643		
DB	646	ACCTCATTAACAGAG-ACCACATGACAAAGACACACACACACACACACACACACAC	588		
QY	2644	ACTGAGAGCAGATGAG	2703		
DB	587	ACTGAGAGCAGATGAG	528		
QY	2704	CTACAGTGGAGAC	2763		
DB	527	CTACAGTGGAGAC	468		
QY	2764	TTCCGAGACACATGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2823		
DB	467	TTCCGAGACACATGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	408		
QY	2824	CTCCCATCCATGAG	2883		
DB	407	CTCCCATCCATGAG	348		
QY	2884	AGCCCCCGCCAC	2943		
DB	347	AGCCCCCGCCAC	288		
QY	2944	TGGAGAGCCTGGAG	3002		
DB	287	TGGAGAGCCTGGAG	228		
QY	3003	CTGCAAGAACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3062		
DB	227	CTGCAAGAACTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	168		
QY	3063	GACCACTGGAGTGGACACTGAGTGGACAGAGAGAGAGAGAGAGAGAGAGAGAG	3122		
DB	167	GACCACTGGAGTGGACACTGAGTGGACAGAGAGAGAGAGAGAGAGAGAGAGAG	108		
QY	3123	TCGAGGCTTATTGTAAGTCTTATTCTTACAAAGAGAGAGAGAGAGAGAGAGAG	3182		
DB	107	TCGAGGCTTATTGTAAGTCTTATTCTTACAAAGAGAGAGAGAGAGAGAGAGAG	48		

QY 3183 CTCCTTAACATCTGCAACAAGAGGCGCTGGATATCAACTTGC 3229
 Db 47 CTCCTTAACATCTGCAACAAGAGGCGCTGGATATCAACTTGC 1

RESULT 2
 AI341249/c 560 bp mRNA EST 15-FEB-1999
 LOCUS qx90d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009767 3',
 DEFINITION mRNA sequence.
 AI341249
 ACCESSION AI341249.1 GI:4078176
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 560)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Jan 14, 1998 this sequence version replaced gi:1798073.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrp/image/image.html

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 Seq primer: -400P from Glibco
 High quality sequence stop: 452.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:2009767"
 /clone_lib="NCI_CGAP_GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker. Plasmid DNA from the normalized library
 NCI_CGAP_GC4 was prepared, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (cloneds 1257096-125861,
 1469064-1470983, and 1473592-1476743). Subtraction by
 Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 102 a 144 c 180 g 133 t 1 others
 ORIGIN

Query Match 17.2% Score 557.4; DB 45; Length 560;
 Best Local Similarity 99.6% Pred. No. 1.5e-120;
 Matches 558; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2670 CATTTAAAAATCAGTCGATCGAATCCCGACCTACGTGGAACAACAGAGCCCTC 2729
 Db 560 CATTTAAANATCAGTCGATCGAATCCCGACCTACGTGGAACAACAGAGCCCTC 501

QY 2730 TCGAACAATGCAAGATCCTATAGAGATATATAACTCTCCAGAACATCCAGCGTCGGCT 2789
 Db 500 TCGAACAATGCAAGATCCTATAGAGATATATAACTCTCCAGAACATCCAGCGTCGGCT 441

QY 2790 GTCCCTCAGCTCCCGCCTCCGCCACGAGCGCTTACTCTCCATCCATCGGAGGCGTGGAGCG 2849

Db 440 GTCCCTCAGCTCCCGCCTCCCGCCTACGACAGCGCTACCTCCATCGAGGCGGTAAAGCG 381

QY 2850 CAGCTGTGTCAGGCCCTGTGCTGACGCCCGCCAGCGCCCGCCACAGACATGTGCCAC 2909
 Db 380 CAGCTGTGTCAGGCCCTGTGCTGACGCCCGCCAGCGCCCGCCACAGACATGTGCCAC 321

QY 2910 CTCCTTCGAGTCATGATGTCTCGGGCCTGTAAAGGTGGAGGCGCTGGCCCGGGCCTCC 2969
 Db 320 CTCCTTCGAGTCATGATGTCTCGGGCCTGTAAAGGTGGAGGCGCTGGCCCGGGCCTCC 261

QY 2970 CCGTGACAGAACCCACACTGCGGCGGAGAGGGGTCTGTGCAGAAACACTGTGCGCTGTG 3029
 Db 260 CCGTGACAGAACCCACACTGCGGCGGAGAGGGGTCTGTGCAGAAACACTGTGCGCTGTG 201

QY 3030 CGGAGAGCTGGGCGACCATGCGCTGTGCGCTCTCAGACACTCGGATGAGCTGTGAGC 3089
 Db 200 CGGAGAGCTGGGCGACCATGCGCTGTGCGCTCTCAGACACTCGGATGAGCTGTGAGC 141

QY 3090 AGGACGGCGCAGGCGGAGAGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGAGT 3149
 Db 140 AGGACGGCGCAGGCGGAGAGCTGTGCGCTGTGCGCTGTGCGCTGTGAGT 81

QY 3150 TCTTCAAAAAGAGAGAAAGGAAATGGAGCGCTTCTTAACATCTGCACAAAGAGAG 3209
 Db 80 TCTTCAAAAAGAGAGAAATGGAGCGCTTCTTAACATCTGCACAAAGAGAG 21

QY 3210 CGCTGGATATCAACTTGC 3229
 Db 20 CGCTGGATATCAACTTGC 1

RESULT 3
 AI937563/c 416 bp mRNA EST 06-SEP-1999
 LOCUS wp/8q11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467940 3',
 DEFINITION similar to TR:075975 075975 GABA-B RECEPTOR SPLICED VARIANT 2 ;,
 mRNA sequence.
 AI937563
 ACCESSION AI937563.1 GI:5676433
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 416)
 AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/RTGAP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3187952.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrp/image/image.html

Seq primer: -400P from Glibco.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:2467940"
 /clone_lib="NCI_CGAP_Brn25"
 /tissue_type="anaplastic oligodendroglioma"

FEATURES
 source

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/lab_host="DH10b"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGGCGCGCATGAGTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT      72 a 127 c 130 g      86 t      1 others
ORIGIN

Query Match      12.6%; Score 410.2; DB 63; Length 416;
Best Local Similarity 99.0%; Pred. No. 4; 7e-85;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 356 CCCACGCCCGACGCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGTCTGGG 297
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QY 3054 GCCTCTGAGCACTCGGATGACACTAGTGTGACAGAGCGGGGAGAGACTTGG 3113
DB 176 GCCTCTGAGCACTCGGATGACACTAGTGTGACAGAGCGGGGAGAGACTTGG 117
QY 3114 CACCTGACCTGAGCCTTATTGTGAAGTCTCTTATTCTTACAAAGAGAGAAAGGAA 3173
DB 116 CACCTGACCTGAGCCTTATTGTGAAGTCTCTTATTCTTACAAAGAGAGAAAGGAA 57
QY 3174 ATGGGACGCTCTTCTTAAACATCTGCAGAACAGAGGCGCTGGATATCAAACTTGC 3229
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RESULT 4
A1500214/c 414 bp mRNA EST 14-APR-1999
LOCUS tm4a05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165744 3',
DEFINITION mRNA sequence.
ACCESSION A1500214
VERSION A1500214.1 GI:4392196
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRNAP). Tumor Gene Index
COMMENT Unpublished (1998)
On Mar 20, 1998 this sequence version replaced gi:2980163.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
```

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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
www.bio.lnlnl.gov/bnbp/image/image.html

Insert Length: 506 Std Error: 0.00
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FEATURES
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                /lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGGCGCGCATGAGTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT      74 a 127 c 128 g      84 t      1 others
ORIGIN

Query Match      12.6%; Score 408.2; DB 47; Length 414;
Best Local Similarity 99.0%; Pred. No. 1; 4e-85;
Matches 410; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2816 ACCTTACCTCCATCCATCGGAGGCGTGTGTGACAGCCCTGCTGCTGAGCC 2875
DB 414 ACCTTACCTCCATCCATCGGAGGCGTGTGTGACAGCCCTGCTGCTGAGCC 355
QY 2876 CCACGCCCGACGCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGTCTGCGGCC 2935
DB 354 CCACGCCCGACGCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGTCTGCGGCC 295
QY 2936 TGTAAAGGTGGAGGCGCTGGGCGCCGCGGCTCCCGCTGACAGAACACACTGGGCGAG 2995
DB 294 TGTAAAGGTGGAGGCGCTGGGCGCCGCGGCTCCCGCTGACAGAACACACTGGGCGAG 235
QY 2996 GGGTCTGTGCAAAACACTGTGCGCTGTGCTGTGCGAGAGCTGGGACCATGGCTGGC 3055
DB 234 GGGTCTGTGCAAAACACTGTGCGCTGTGCTGTGCGAGAGCTGGGACCATGGCTGGC 175
QY 3056 CTCTCAGACACACTCGGATGACACTCAGTGTGACAGAGGCGGAGGAGAGACTTGCA 3115
DB 174 CTCTCAGACACACTCGGATGACACTCAGTGTGACAGAGGCGGAGGAGAGACTTGCA 115
QY 3116 CCTGACCTGAGCCTTATTGTGAAGTCTCTTATTCTTACAAAGAGAGAGAGGAAT 3175
DB 114 CCTGACCTGAGCCTTATTGTGAAGTCTCTTATTCTTACAAAGAGAGAGGAAT 55
QY 3176 GGGAGCTCTTCTTAAACATCTGCAGAACAGAGGCGCTGGATATCAAACTTGC 3229
DB 54 GGGAGCTCTTCTTAAACATCTGCAGAACAGAGGCGCTGGATATCAAACTTGC 1

RESULT 5
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LOCUS ap29g06.x1 Schiller astrocytoma Homo sapiens cDNA clone
DEFINITION IMAGE:1956826 3' similar to TR:008621 008621 GABA-BRIB RECEPTOR. ;,
mRNA sequence.
ACCESSION A1214087
VERSION A1214087.1 GI:3777688
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 397)	Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Thasing, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: polyp not found Seq primer: -40UP from Gibco High quality sequence stop: 375.	Unpublished (1997) On Jan 17, 1998 this sequence version replaced gi:1900223.	
1	Eutheria; Primates; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Chordata; Craniata; Homidae; Homo.			
1	1 (bases 1 to 397)			
1	Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Thasing, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.			
1	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: polyp not found Seq primer: -40UP from Gibco High quality sequence stop: 375.			
1	Location/Qualifiers			
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1	/db_xref="taxon:9606"			
1	/clone="IMAGE:1956826"			
1	/clone_lib="Schiller astrocytoma"			
1	/sex="male"			
1	/tissue_type="astrocytoma"			
1	/dev_stage="44 years"			
1	/lab_host="SOLR"			
1	/note="Organ: brain; Vector: pluescript SK- (Stratagene); Site:1: ECoRI; Site:2: XhoI; Double-stranded cDNA was prepared from human astrocytoma using primer 5'-GAGAGAGAGAGAGAGAGAACTGCTGACT(18)-3'. An ECoRI adaptor was used on the 5' end of the cDNA as follows: 5'-ATTGCGCAGCAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."			
BASE COUNT	109 a 109 c 115 g 64 t			
ORIGIN				
Query Match	12.0%; Score 389.8; DB 43; Length 397;			
Best Local Similarity	99.5%; Pred. No. 2.9e-81;			
Matches 391: Conservative	0; Mismatches 2; Indels 0; Gaps 0;			
1147	AAGCGGTACGGGCTGGGGCCAGCAAGTTCACAGGGTACGGCTAGATGGCATTGGGTC	1206		
Db	5 AAGCGGTACGGGCTGGGGCCAGCAAGTTCACAGGGTACGGCTAGATGGCATTGGGTC	64		
1207	ATCGCCAGACACTGCAGAGGGCCATGAGAACTCATGCTCCAGCAGCCGGACAGCGG	1266		
Db	65 ATCGCCAGACACTGCAGAGGGCCATGAGAACTCATGCTCCAGCAGCCGGACAGCGG	124		
1267	ATCCAGAGACTTCACTACAGGACACACAGCGTGGGCGAGATCATCTCCATGCATGAAC	1326		
Db	125 ATCCAGAGACTTCACTACAGGACACACAGCGTGGGCGAGATCATCTCCATGCATGAAC	184		
1327	GAGACCACTTCTTGGGGTCAACGGGTCAAGTTGATTCCGGAATGGGAGAAATGGG	1386		
Db	185 GAGACCACTTCTTGGGGTCAACGGGTCAAGTTGATTCCGGAATGGGAGAAATGGG	244		
1387	ACCATTAAATTTACTCAATTCGAAGACACAGGAGGTGAAGTGGGAGATGCAACGCT	1446		
Db	245 ACCATTAAATTTACTCAATTCGAAGACACAGGAGGTGAAGTGGGAGATGCAACGCT	304		
1447	GTGGCGACACACTGGAGATCATCATGACACCATGAGTTCCAGAGATCCGAAACACCA	1506		

```

Db      305 GTGGCCGACAGACTGCATCATCATCAATGACCACCTCAGCGTTTCCAAGATCCGAACACACA   364
QY      1507 AAAGACAAGACCATTATCTGTGGAGCAGTCGGG    1539
|||||
Db      365 AAAACAAGAACCATCATCTGTGGAGCAGTGCGG    397
|||||

RESULT      6
AI000006/c          384 bp       mRNA           EST         05-JUN-1998
LOCUS              rRNA sequence.
DEFINITION        AT000006 Homo sapiens cDNA clone IMAGE:1613751 3',
VERSION           AT000006.1 GI:3190560
KEYWORDS          ESR.
SOURCE            human.
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE          1 (bases 1 to 384)
AUTHORS            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                  Tumor Gene Index
JOURNAL            Unpublished (1997)
COMMENT            On Jan 17, 1998 this sequence version replaced gi:1900928.
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNU at:
www.bio.linn.gov/bdnp/image/image.html

FEATURES             source
                     location/Qualifiers
                     .....,..
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1613751"
                     /clone_lib="NCI-CGAP_Gc3"
                     /tissue-type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pR173D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pR173
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT          72 a     116 c     116 g     80 t

ORIGIN
Query Match          11.4%; Score 368.2; DB 40; Length 384;
Best Local Similarity 99.0%; Pred. No. 3.3e-76;
Matches 381; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Db 265 CTCGCCCTGACGAACACACTGGGAGAGGGTCTGCTGCAGAAACACTGCTGCTCT 206

QY 3025 GGCTGGGAGAAAGCTGGGACCATGCTGCTTCAGAGACCATCGATGGACCTCAGG 3084

Db 205 GGCTGGGAGAAAGCTGGGACCATGCTGCTTCAGAGACCATCGATGGACCTCAGG 146

QY 3085 TGGACAGGACGGGGGAGGAGGAGTGGACCTGACCTCGAAGCTTATTTGTGAAGTCC 3144

Db 145 TGGACAGGACGGGGGAGGAGGAGTGGACCTGACCTCGAAGCTTATTTGTGAAGTCC 86

QY 3145 TTTATTTCTTCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3204

Db 85 TTTATTTCTTCAAAAAG 26

QY 3205 GGAGGCGCTGGGATATCAACTTGC 3229

Db 25 GGAGGCGCTGGGATATCAACTTGC 1

RESULT 7

LOCUS H1451/c 371 bp mRNA EST 10-JUL-1995

DEFINITION YMG2d04.r1 Soares adult brain NZB4HB55Y Homo sapiens cDNA clone IMAGE:163495 5', mRNA sequence.

ACCESSION H1451

VERSION H1451.1 GI:878971

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 371)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT On Sep 21, 1992 this sequence version replaced gi:279426.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Insert Size: 1720

High quality sequence stops: 229

Source: IMAGE Consortium, LUNL

This clone is available royalty-free through LUNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1720 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 229.

FEATURES

Source

1..371

/organism="Homo sapiens"

/db_xref="GDB:583464"

/db_xref="taxon:9606"

/clone="IMAGE:163495"

/clone_lib="Soares adult brain NZB4HB55Y"

/sex="Male"

/dev_stage="55-year old"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: brain; Vector: pTZ19 (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento

Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

BASE COUNT 60 a 99 c 106 g 99 t 7 others

ORIGIN

Query Match 11.0%; Score 355.6; DB 22; Length 371;
Best Local Similarity 97.0%; Pred. No. 3e-73; Indels 0; Gaps 0;
Matches 358; Conservative 0; Mismatches 11;

QY 968 AGAGCCTTCTTGGTGGAGACAGTGCACACGAGAACCACTCATCCGCTCCCGGA 1027

Db 369 AGCAGCCTTCTTGGTGGAGAGTGCACACGAGAACCACTCATCCGCTCCCGGA 310

QY 1028 AGAATCGCTTGTGCTGATGAGAGGCTACATGGCTGATTTCCAGGCCCTGAGCTCCA 1087

Db 309 AGAATCGCTTGTGCTGATGAGAGGCTAAATTGCTGATTTCCAGGCCCTGAGCTCCA 250

QY 1088 AGCAGATCAAGACCATCTCAGAAAGACTCCACAGCAGTATGAGAGAGTACACACA 1147

Db 249 AGCAGATCAAGACCATCTCAGAAAGACTCCACAGCAGTATGAGAGAGTACACACA 190

QY 1148 AGCGGTGAGCGGTGGGGCCCGCAGCAAGTTCACAGGGTATGCTTACATGGCATCGGTCA 1207

Db 189 AGCGGTGAGCGGTGGGGCCCGCAGCAAGTTCACAGGGTATGCTTACATGGCATCGGTCA 130

QY 1208 TCGCCCAAGACACTGACAGAGGGCCATGAGACACTGCTATCCGACGCGGACCGGA 1267

Db 129 TCGCCCAAGACACTGACAGAGGGCCATGAGACACTGCTATCCGACGCGGACCGGA 70

QY 1268 TCCAGACTTCAACTACAGACACACACCGCTGGGACATCTCATGTCATGCAAGC 1327

Db 69 TCCAGACTTCAACTACAGACACACACCGCTGGGACATCTCATGTCATGCAAGC 10

QY 1328 AGACCAACT 1336

Db 9 AGACCAACT 1

RESULT 8

LOCUS Z39716/c 326 bp mRNA EST 07-NOV-1994

DEFINITION HSCIHH042 normalized infant brain cDNA Homo sapiens cDNA clone c-1bh04 3', mRNA sequence.

ACCESSION Z39716

VERSION Z39716.1 GI:565511

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 326)
Aulicay, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houligatte, R., Juneau, M.N., Lamy, B., Lorenzani, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouliot, Y., Sebastiani-Kabakchis, C. and Tessier, A.

TITLE IMAGE: molecular integration of the analysis of the human genome and its expression

JOURNAL Genet. Res. 66 (1995)

MEDLINE 95277534

COMMENT Contact: Genethon
Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, Bp60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698

Email: genexpress@genethon.fr
Single read, 27 T removed at sequence 5' end
Genexpress_library_id: C; Genexpress_sequence_id: alc-1hh04
Seq primer: (-21)M13-universal.

FEATURES

source

1..326
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C-1hh04"
/clone_lib="normalized infant brain cdna"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

BASE COUNT 62 a 103 c 88 g 69 t 4 others
ORIGIN

Query Match 9.9%; Score 320.4; DB 20; Length 326;
Best Local Similarity 98.5%; Pred. No. 5.2e-65;
Matches 321; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2904 GCCACCTCCCTCCGAGTACGTGCTCGGGCCTGAAGGTGGGAGCCTGGGCCCGGGG 2963
|||||
Db 326 GCCACCTCCCTCCGAGTACGTGCTCGGGCCTGAAGGTGGGAGCCTGGGCCCGGGG 267
QY 2964 CCTCCCCCGTGACAGAACACACTGGGCGAGGGGTCTGCTGAGAAACACTGTGGCTC 3023
|||||
Db 266 CCTCCCCCGTGACAGAACACACTGGGCGAGGGGTCTGCTGAGAAACACTGTGGCTC 207
QY 3024 TGGCTCGGAGAGCTGGGACCATGGCTGCTCTCAGAGCACTGGATGGCACTCAG 3083
|||||
Db 206 TGGCTCGGAGAGCTGGGACCATGGCTGCTCTCAGAGCACTGGATGGCACTCAG 147
QY 3084 GTGGAGAGGAGCGGGGAGGGGAGACTTGGCACTCACTCGAGCTTTTGTGAAGTC 3143
|||||
Db 146 GTGGAGAGGAGCGGGGAGGGGAGACTTGGCACTCACTCGAGCTTTTGTGAAGTC 87
QY 3144 CTATTCTTCAACAAGAGAGAGAAATGAGAGCTTCTCTTAACATCTGCAACA 3203
|||||
Db 86 CTATTCTTCAACAAGAGAGAGAAATGAGAGCTTCTCTTAACATCTGCAACA 27
QY 3204 AGGAGCGCTGGGATATCAAACTTGC 3229
|||||
Db 26 AGGAGCGCTGGGATATCAAACTTGC 1

RESULT 9
243654 341 bp mRNA EST 14-NOV-1994
LOCUS HSC1H041 normalized infant brain cdna Homo sapiens cdna clone
DEFINITION c-1hh04, mRNA sequence.
ACCESSION 243654
VERSION 243654.1 GI:572828
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 341)
AUTHORS Auffray,C., Benar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houligatte,R., Junneau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabackis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome
and its expression

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, Bp60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr

COMMENT

Genexpress_library_id: C; Genexpress_sequence_id: ylc-1hh04
Seq primer: (-21)M13-universal.

FEATURES

source

1..341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C-1hh04"
/clone_lib="normalized infant brain cdna"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

BASE COUNT 87 a 102 c 83 g 66 t 3 others
ORIGIN

Query Match 9.7%; Score 315; DB 20; Length 341;
Best Local Similarity 98.8%; Pred. No. 9.8e-64;
Matches 337; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 2191 GGGATGAGTGTCTCAACAGTGGGATCATGCAATCGGGGCGGTGCTCCTTCTG 2250
|||||
Db 1 GGGATGAGTGTCTCAACAGTGGGATCATGCAATCGGGGCGGTGCTCCTTCTG 60
QY 2251 ACCGGGAGCAGCCCAATGTGCACTTGTGATCGTGGCTGTGTCATCATCTTGCAGC 2310
|||||
Db 61 ACCGGGAGCAGCCCAATGTGCACTTGTGATCGTGGCTGTGTCATCATCTTGCAGC 120
QY 2311 ACCATCACCTCTGCTGCTGATTTGTGCGGAAGTCAATCACTGAGACAAACAGAT 2370
|||||
Db 121 ACCATCACCTCTGCTGCTGATTTGTGCGGAAGTCAATCACTGAGACAAACAGAT 180
QY 2371 GCAGCAAGCAG-AACAGGGATTCAGTTCACGACAGAAATCAGAAAGAAAGATTCTTA 2429
|||||
Db 181 GCAGCAAGCAGAAACAGGGGATTCAGTTCACGACAGAAATCAGAAAGAAAGATTCTTA 240
QY 2430 AAGCTCACCTGGTCAACAGTGTGAACCAAGCAGCAATCCGGCT-GGAGGGCTAC 2488
|||||
Db 241 AAGCTCACCTGGTCAACAGTGTGAACCAAGCAGCAATCCGGCTGGAGAGGGCTAC 300
QY 2489 AGTCAGAAAACCATCGCTGCGAATGAAGTACACAGAGCTG 2529
|||||
Db 301 AGTCAGAAAACCATCGCTGCGAATGAAGTACACAGAGCTG 341

RESULT 10
T07621 368 bp mRNA EST 30-JUN-1993
LOCUS EST05111 Fetal brain, Striatum (cat#936206) Homo sapiens cdna
DEFINITION clone HFBEL81, mRNA sequence.
ACCESSION T07621
VERSION T07621.1 GI:318770
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE	Eutheria: Primates: Catarrhini: Hominoidea: Homo.
AUTHORS	1 (bases 1 to 368)
TITLE	Adams,M.D., Kerlavage,A.R., Fields,C. and Venter,J.C. 3,400 expressed sequence tags identify diversity of transcripts from human brain
JOURNAL	Nature Genet. 4, 256-267 (1993)
MEDLINE	93364420
COMMENT	Contact: Adams, MD The Institute for Genomic Research 932 Clopper Road, Gathersburg, MD 20878 Tel: 3018699036 Fax: 3018699423 Email: mdadams@tigr.org Seq primer: M13-21. Location/Qualifiers 1..368
FEATURES	/organism="Homo sapiens" /db_xref="ATCC (Inhost):84252" /db_xref="taxon:9606" /clone="HBEL81" /clone_lib="Fetal brain, Striatum (cat#936206)" /note="Vector: LambdaZAP-II; 17-18 wk gestation, female; oligo-dr + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average insert size." BASE COUNT 91 a 94 c 79 g 101 t 3 others
ORIGIN	
Query Match	8.0%; Score 258; DB 20; Length 368;
Best Local Similarity	94.8%; Pred. No. 2,5e-50;
Matches 289; Conservative	0; Mismatches 11; Indels 5; Gaps 2
OY 1543	ATCTCCTACCTCTCTACAGATCCTCTGCCCCACCATCCTCGGGATGCATGCC 1602
Dd 1	ATCTCCTACCTCTCTACAGATCCTCTGCCCCACCATCCTCGGGATGCATGCC 60
OY 1603	AGTGTTCCTCTCTCAACATCAAGCCGAATCAGAAGCTATAAGATGTCAGT 1662
Dd 61	AGTGTTCCTCTCTCAACATCAAGCCGAATCAGAAGCTATAAGATGTCAGT 120
OY 1663	CCATCATGAAACAACCTTATCATCCTTGAGGGAGTCTTCATGCTTCATATTTC 1722
Dd 121	CCATCATGAAACAACCTTATCATCCTTGAGGGAGTCTTCATGCTTCATATTTC 180
OY 1723	TTTGCCCTTGATGATCTTTGTCTCGAAAACCTTTGAAACACTTTGCACCGTCAG 1782
Dd 181	TTTGCCCTTGATGATCTTTGTCTCGAAAACCTTTGAAACACTTTGCACCGTCAG 240
OY 1783	ACCT-GGATTCACACCGGAGCT----ACAGAACCGCTTTTGAGGGCATGTTGCAAGA 1837
Dd 241	ACCTGGATTCACACCGGAGCTTACACGAGACCGCTTTTGAGGGCATGTTGCAAGA 300
OY 1838	CCTGG 1842
Dd 301	CCTGG 305
RESULT 11	
AA324303	
LOCUS	283 bp mRNA EST 20-APR-1997
DEFINITION	EST227126 Cerebellum II Homo sapiens CDNA 5' end, mRNA sequence.
ACCSSION	AA324303
VERSION	AA324303.1 GI:1975568
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 283) Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wa,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

LOCUS	AA613872/c	235 bp	mrna	EST	18-FEB-1998
DEFINITION	no81106.s1	NCI_GCAP	A41 Homo sapiens	CDNA clone IMAGE:1113251	3'
FEATURES	<p>source location/Qualifiers</p> <p>1..283</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="ATCC (inhost):124801"</p> <p>/db_xref="taxon:9606"</p> <p>/clone_lib="Cerebellum II"</p> <p>/tissue_type="cerebellum"</p> <p>/dev_stage="adult"</p> <p>/note="Organ: brain; Vector: pbluescript SK-; Site-1: EcoRI; Site-2: XhoI"</p> <p>Base Count 59 a 82 c 75 g 64 t 3 others</p> <p>ORIGIN</p>				
BASE COUNT	59 a 82 c 75 g 64 t 3 others				
ORIGIN					
Query Match	7.5%; Score 241.8; DB 31; Length 283;				
Best Local Similarity	93.7%; Pred. No. 1,4e-46;				
Matches 268; Conservative 0; Mismatches 10; Indels 2; Gaps 2;					
OY 1890	GAGAAATACAGCATGAGCGGACGACCACAGAGAGGAGATATTCATCCGCTCTCTG 2049				
Db 1	GAGAGATACAGCATGAGCGGACGACCACAGAGAGGAGATATTCATCCGCTCTCTG 60				
OY 2050	GAGCACTGTGAGAACCCCATATGACCATCTGGCTTGGCATGCTTATGCTTCAAGGA 2109				
Db 61	GAGCACTGTGAGAACCCCATATGACCATCTGGCTTGGCATGCTTATGCTTCAAGGA 120				
OY 2110	CTTCTCATGTTGGTGGTGTCTTCTTACCTTGGGAGACCCGCAACGTCACATCCCGGA 2169				
Db 121	CTTCTCATGTTGGTGGTGTCTTCTTACCTTGGGAGACCCGCAACGTCACATCCCGGA 180				
OY 2170	CTCAACGACAGCAATACATCGGATGAGTGTCTACAACGT-GGGATCATGTGCATCAT 2228				
Db 181	CTCAACGACAGCAATACATCGGATGAGTGTCTACAACGTCGAGGTCATGTGCATCAT 240				
OY 2229	CGGGGGCGG-C-TGTCTCTTCTGACCCGGGACAGCCCA 2267				
Db 241	CGGGGGCGGCTTGTCTTCTCTGACCCGGGACAGCCCA 280				
RESULT 12					
AA613872/c					

mRNA sequence.
 AA613872
 VERSION
 AA613872.1 GI:2466006
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 235)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 TITLE
 Unpublished (1997)
 JOURNAL
 On May 18, 1995 this sequence version replaced gi:811266.
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.
 cDNA Library Arraying: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 687 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 228.
 Location/Qualifiers
 1..235
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:113251"
 /clone_lib="NCI-CGAP_AAL"
 /tissue_type="adrenal adenoma"
 /lab_host="SOLR (kanamycin resistant)"
 /notes="Organ: adrenal gland; Vector: Bluescript SK-;
 Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
 Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5'
 adaptor sequence: 5' GAATTCGACGAG 3' 3' adaptor
 sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' Average insert
 size: 1.6 kb.
 45 a 73 c 58 g 59 t

BASE COUNT
 ORIGIN
 Query Match 7.2%; Score 235; DB 36; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-45; Indels 0; Gaps 0;
 Matches 235; Conservative 0; Mismatches 0;
 QY 2973 TGACAGAACACACTGGGAGAGGGTCTGCTCGAGAAACACTGTGGCTGTGGCTGGCG 3032
 Db 235 TGACAGAACACACTGGGAGAGGGTCTGCTCGAGAAACACTGTGGCTGTGGCTGGCG 176
 QY 3033 AGAGCTGGGACCACTGGCTGTGGCTCTCAGGACCACTCGGATGGCACTCAGTGGACAGG 3092
 Db 175 AGAGCTGGGACCACTGGCTGTGGCTCTCAGGACCACTCGGATGGCACTCAGTGGACAGG 116
 QY 3093 ACGGGGACGGGGAGAGCTTGGCACTTGGCACTCGAGGCTTATTGTGAAGTCTCTTATTCT 3152
 Db 115 ACGGGGACGGGGAGAGCTTGGCACTTGGCACTCGAGGCTTATTGTGAAGTCTCTTATTCT 56
 QY 3153 TCACAAAGAGAGAACGGAATGGGACGCTCTTCCATTACATCTGCAACAAGGA 3207
 Db 55 TCACAAAGAGAGAACGGAATGGGACGCTCTTCCATTACATCTGCAACAAGGA 1

RESULT 13
 AQ744524
 LOCUS
 DEFINITION HS_5508_A1_D10_17A RPCI-11 Human Male BAC Library Homo sapiens
 853 bp DNA GSS 16-JUL-1999

genomic clone Plate-1084 Col-19 Row-G, genomic survey sequence.
 AQ744524
 VERSION
 AQ744524.1 GI:5522046
 GSS.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 853)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Kellier, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589
 CONTACT: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (<http://info@resgen.com>). BAC end Web Server:
<http://www.htsc.washington.edu>
 Plate: 1084 row: G column: 19
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 853.
 Location/Qualifiers
 1..853
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate:1084 Col=19 Row=G"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
 224 a 211 c 200 g 215 t 3 others

BASE COUNT
 ORIGIN
 Query Match 6.9%; Score 223.6; DB 87; Length 853;
 Best Local Similarity 94.2%; Pred. No. 4.5e-42;
 Matches 243; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
 QY 1095 CAAGACCATCTCAGGAAGACTCCACAGCAGTATGAGAGAGTACACACAG-CGGT 1153
 Db 465 CAATCCCTGTTTTCAGACTCCACAGCAGTATGAGAGAGTACACACAGCCGGC 524
 QY 1154 CAGCGCTGGGGCCAGCAAGTTCCACGGGTAGCCCTACGATGGCATCTGGGTCTATCGCCA 1213
 Db 525 CAGCGCTGGGGCCAGCAAGTTCCACGGGTAGCCCTACGATGGCATCTGGGTCTATCGTCA 584
 QY 1214 AGACATGACAGGGCCATGGAGACACTGCTGACAGAGCCGGCACCAGCGGATCCAGG 1273
 Db 585 AGACATGACAGGGCCATGGAGACACTGCTGACAGAGCCGGCACCAGCGGATCCAGG 644
 QY 1274 ACTTCAACTACAGGACCAACAGCTGGGAGGATCATCTCAATGCCATGAACAGACCA 1333
 Db 645 ACTTCAACTACAGGACCAACAGCTGGGAGGATCATCTCAATGCCATGAACAGACCA 704
 QY 1334 ACTTCTTCGGGGTTCACGG 1351
 Db 705 ACTTTTTCGGGGTTCACGG 722

RESULT 14
 AW138313/c
 LOCUS
 DEFINITION AW138313 136 bp mRNA EST 29-OCT-1999

DEFINITION UI-H-B11-acz-e-12-0-UI_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2716127 3', mRNA sequence.
ACCESSION AW138313
VERSION AW138313.1 GI:6142631
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 136)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jul 9, 1999 this sequence version replaced gi:5433571.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
source Location/Qualifiers
1..136
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2716127"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI-CGAP_Sub3 library is a subtracted library derived from
the NCI-CGAP_Sub1 library, which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI-CGAP libraries:
NCI-CGAP_Co4, NCI-CGAP_Pr22, NCI-CGAP_Pr28, NCI-CGAP_Co10,
NCI-CGAP_Co16, NCI-CGAP_Kid5, NCI-CGAP_Kid12,
NCI-CGAP_Kid3, NCI-CGAP_Kid11, NCI-CGAP_Lym2,
NCI-CGAP_Br2, NCI-CGAP_Co8, NCI-CGAP_CLL1, NCI-CGAP_Lei2,
NCI-CGAP_Brn23, NCI-CGAP_Lu5, NCI-CGAP_Lu24,
NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_GC6,
NCI-CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI-CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911,
1456008-1456775, 1500852-1502855); NCI-CGAP_Kid5 pool 1
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI-CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439); NCI-CGAP_GC4
pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI-CGAP_Pr22 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759,
1101192-1101959, 1217928-1220615); NCI-CGAP_Co10 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255,
1144584-1145351). Subtraction was performed as previously
described [Bonaldo, Lennon & Soares (1996): Normalization
and Subtraction: Two Approaches To Facilitate Gene
Discovery. Genome Research 6, 791-806.
TAG_LIB=NCI-CGAP_Brn26
TAG_TISSUE=brain
TAG_SEQ=ATAGG"
30 a 28 c 27 g 51 t
BASE COUNT
ORIGIN

Query Match 4.1%; Score 134; DB 69; Length 136;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3111 TGGCACCCTGACCTCGAGCCCTATTGCTGAAGTCCTATTCTTCACAAAGAGGAAGCG 3170
|||||
Db 136 TGGCACCCTGACCTCGAGCCCTATTGCTGAAGTCCTATTCTTCACAAAGAGGAAGCG 77
|||||
QY 3171 GAAATGGGACGCTCTTCAACATCTGCAAAACAGGAGCGCTGGGATATCAAACTTGCA 3230
|||||
Db 76 GAAATGGGACGCTCTTCAACATCTGCAAAACAGGAGCGCTGGGATATCAAACTTGCA 17
|||||
QY 3231 AAAAAAAAAAAAAA 3244
|||||
Db 16 AAAAAAAAAAAAAA 3
RESULT 15
AA022569/c
LOCUS ze70h11.r1 Soares fetal heart_NDHH19W Homo sapiens cDNA clone
DEFINITION IMAGE:364389 5', mRNA sequence.
ACCESSION AA022569
VERSION AA022569.1 GI:1486659
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 302)
Hallier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.,
and Warra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 984 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 136.
Location/Qualifiers
1..302
/organism="Homo sapiens"
/db_xref="GDB:1281093"
/db_xref="taxon:9606"
/clone="IMAGE:364389"
/clone_lib="Soares_fetal_heart_NDHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I-oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTTTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot -5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung

```
BASE COUNT      60 a      92 c      97 g      46 t      7 others
ORIGIN

Query Match      4.1%; Score 132.2; DB 27; Length 302;
Best Local Similarity 82.2%; Pred. No. 7.8e-21;
Matches 175; Conservative 0; Mismatches 32; Indels 6; Gaps 2;

QY 56 GGGATTGCCCGACAT-CCTTCAGCGAAGTGCATGTGTGTTGTAACCA-----TCGTT 109
Db 302 GGGATTGCCCGACATCCCTTCAGCGAAGTGCATGTGTGTTGTAACCACTCGGTGGC 243
QY 110 GGCTGTCCGGAGACCGCGAGACCGGTCCAGGCTGCGGGGAGTCGAGGCGGAGGAGAG 169
Db 242 TTGTCNGGGAGACCGCGAGGACCGGTCCAGGCTGCGGGGTAGTCGAGGCGGAGGAGAG 183
QY 170 GCCCGGTAGTGACGACAGTCCAGAGCCGTGCGCCCCCAGAACTGCGGTCGCCCGCGTG 229
Db 182 GCCCGGTAGTGACGACAGTCCAGAGCCGTGCGCCCCCAGAACTGCGGTCGCCCGCGTG 123
QY 230 CACCCCGCGCGCGCATGCCCGAGTTGCCCGCGC 262
Db 122 ACCCCCTGNGCGCATGCCCGAGTTGCCCGCGC 90
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Search completed: March 16, 2000, 11:46:08
Job time: 1875 sec

Matches		887; Conservative	3; Mismatches	1; Indels	0; Gaps	0;
Db	51	PSSPPLSINGMLPLTKEVAKSIGRGVLP	PAVELAEIQIRNESLLRPYFLDLRLYDTECDN	110		
QY	8	SATGPLSINGMLPLTKEVAKSIGRGVLP	PAVELAEIQIRNESLLRPYFLDLRLYDTECDN	67		
Db	111	AKGLKAFYDAIKYGNHLMVFGGVCPSVTSII	ABESLOGNVLVQSFATTPVLADKKKYP	170		
QY	68	AKGLKAFYDAIKYGNHLMVFGGVCPSVTSII	ABESLOGNVLVQSFATTPVLADKKKYP	127		
Db	171	YFRTVPSDNVNPAILKLLKHQWKRVGTLTQD	VQRFSEVRNDLTGLYGEDIEISDTE	230		
QY	128	YFRTVPSDNVNPAILKLLKHQWKRVGTLTQD	VQRFSEVRNDLTGLYGEDIEISDTE	187		
Db	231	SFSNDPCTSVKLLKGNVRIILGQFDQNM	AAKVFCCAYEENMYGSKYQWIIPGWYEPSW	290		
QY	188	SFSNDPCTSVKLLKGNVRIILGQFDQNM	AAKVFCCAYEENMYGSKYQWIIPGWYEPSW	247		
Db	291	EQVHTEANSSCLRNKLLAAMEGYIGVD	FEPLSSKQIKTISGKTPQOQYEREYNNKRSVG	350		
QY	248	EQVHTEANSSCLRNKLLAAMEGYIGVD	FEPLSSKQIKTISGKTPQOQYEREYNNKRSVG	307		
Db	351	PSKFGYAYDGIWIAKTLQAMETLHASS	RHORIQDFNTDHTLGRILLNAMNETNFFG	410		
QY	308	PSKFGYAYDGIWIAKTLQAMETLHASS	RHORIQDFNTDHTLGRILLNAMNETNFFG	367		
Db	411	VTGQVVFNGRGMGTIKFTQDQREVKV	GEYNVADTLEIINDTIRFQSEPPKDKTII	470		
QY	368	VTGQVVFNGRGMGTIKFTQDQREVKV	GEYNVADTLEIINDTIRFQSEPPKDKTII	427		
Db	471	LEQRLKISLPLYSILSALTILGMTIMAS	AFNFNKNQKLIKMSPPYNNLIIIGGMLS	530		
QY	428	LEQRLKISLPLYSILSALTILGMTIMAS	AFNFNKNQKLIKMSPPYNNLIIIGGMLS	487		
Db	531	YASIFLFGLDGVSFYSEKTFETLCTV	RTWILTVGYTTAFGAMFAKTWRVHAIFKNVKKKK	590		
QY	488	YASIFLFGLDGVSFYSEKTFETLCTV	RTWILTVGYTTAFGAMFAKTWRVHAIFKNVKKKK	547		
Db	591	IKDOKLLVIVGGMLLDLCILICQAVD	PLRRTVERYSMEPPDAGRDISIRPLEHCEN	650		
QY	548	IKDOKLLVIVGGMLLDLCILICQAVD	PLRRTVERYSMEPPDAGRDISIRPLEHCEN	607		
Db	651	THMTIWLGIYAYKGLLMFLFCFLAWET	RNVSIIPALNDSKYIGMSVYNGIMCIIGA	710		
QY	608	THMTIWLGIYAYKGLLMFLFCFLAWET	RNVSIIPALNDSKYIGMSVYNGIMCIIGA	667		
Db	711	FLTRDQPNVQFCIVALYIIFCSTITL	CLVFVKLITLRTNPDAATQNRFFQTNQKKED	770		
QY	668	FLTRDQPNVQFCIVALYIIFCSTITL	CLVFVKLITLRTNPDAATQNRFFQTNQKKED	727		
Db	771	SKTSTSVTQSVNQASTSRLEGLOS	ENHRLMKITELDKDLEEVMTQLODTEKTYIKQNH	830		
QY	728	SKTSTSVTQSVNQASTSRLEGLOS	ENHRLMKITELDKDLEEVMTQLODTEKTYIKQNH	787		
Db	831	YOELNDILNLGNFTSTDDGKAILK	NHLDQNPOLQWNTPEPSRTCKDPIEDINSPEHIOR	890		
QY	788	YOELNDILNLGNFTSTDDGKAILK	NHLDQNPOLQWNTPEPSRTCKDPIEDINSPEHIOR	847		
Db	891	RLSLQLPILHHAYLPSIGGV	DASCVPSCVPTASPRHRHVPSPFRVNVSGL	941		
QY	848	RLSLQLPILHHAYLPSIGGV	DASCVPSCVPTASPRHRHVPSPFRVNVSGL	898		
RESULT 2						
ID	088871	PRELIMINARY;		PRT;	940 AA.	
AC	088871;					
DT	01-NOV-1998 (Tremblrel. 08, Created)					
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)					
DT	01-MAY-1999 (Tremblrel. 10, Last annotation update)					
DE	GABA-B RECEPTOR GB2.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;					
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					

RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RA CLARK J.C., LAM A., BONNER T.I.;
RT "gb2, A second GABA-B receptor.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF058795; AAC63994.1; -
DR PFAM; PF00003; 7tmL3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
SQ SEQUENCE 940 AA; 105762 MW; 94C83CC1 CRC32;

Query Match 97.8%; Score 6429; DB 11; Length 940;
Best Local Similarity 97.8%; Pred. No. 0.00e+00;
Matches 871; Conservative 17; Mismatches 3; Indels 0; Gaps 0;

Db	50	PSSPPLSINGMLPLTKEVAKSIGRGVLP	PAVELAEIQIRNESLLRPYFLDLRLYDTECDN	109		
QY	8	SATGPLSINGMLPLTKEVAKSIGRGVLP	PAVELAEIQIRNESLLRPYFLDLRLYDTECDN	67		
Db	110	AKGLKAFYDAIKYGNHLMVFGGVCPSVTSII	ABESLOGNVLVQSFATTPVLADKKKYP	169		
QY	68	AKGLKAFYDAIKYGNHLMVFGGVCPSVTSII	ABESLOGNVLVQSFATTPVLADKKKYP	127		
Db	170	YFRTVPSDNVNPAILKLLKHFRVRVGTLTQ	XQRFSEVRNDLTGLYGEDIEISDTE	229		
QY	128	YFRTVPSDNVNPAILKLLKHQWKRVGTLTQ	DVQRFSEVRNDLTGLYGEDIEISDTE	187		
Db	230	SFSNDPCTSVKLLKGNVRIILGQFDQNM	AAKVFCCAYEENMYGSKYQWIIPGWYEPSW	289		
QY	188	SFSNDPCTSVKLLKGNVRIILGQFDQNM	AAKVFCCAYEENMYGSKYQWIIPGWYEPSW	247		
Db	290	EQVHTEANSSCLRRSLAAMEGYIGVD	FEPLSSKQIKTISGKTPQOQYEREYNNKRSVG	349		
QY	248	EQVHTEANSSCLRRSLAAMEGYIGVD	FEPLSSKQIKTISGKTPQOQYEREYNNKRSVG	307		
Db	350	PSKFGYAYDGIWIAKTLQAMETLHASS	RHORIQDFNTDHTLGRILLNAMNETNFFG	409		
QY	308	PSKFGYAYDGIWIAKTLQAMETLHASS	RHORIQDFNTDHTLGRILLNAMNETNFFG	367		
Db	410	VTGQVVFNGRGMGTIKFTQDQREVKV	GEYNVADTLEIINDTIRFQSEPPKDKTII	469		
QY	368	VTGQVVFNGRGMGTIKFTQDQREVKV	GEYNVADTLEIINDTIRFQSEPPKDKTII	427		
Db	470	LEQRLKISLPLYSILSALTILGMTIMAS	AFNFNKNQKLIKMSPPYNNLIIIGGMLS	529		
QY	428	LEQRLKISLPLYSILSALTILGMTIMAS	AFNFNKNQKLIKMSPPYNNLIIIGGMLS	487		
Db	530	YASIFLFGLDGVSFYSEKTFETLCTV	RTWILTVGYTTAFGAMFAKTWRVHAIFKNVKKKK	589		
QY	488	YASIFLFGLDGVSFYSEKTFETLCTV	RTWILTVGYTTAFGAMFAKTWRVHAIFKNVKKKK	547		
Db	590	IKDOKLLVIVGGMLLDLCILICQAVD	PLRRTVERYSMEPPDAGRDISIRPLEHCEN	649		
QY	548	IKDOKLLVIVGGMLLDLCILICQAVD	PLRRTVERYSMEPPDAGRDISIRPLEHCEN	607		
Db	650	THMTIWLGIYAYKGLLMFLFCFLAWET	RNVSIIPALNDSKYIGMSVYNGIMCIIGA	709		
QY	608	THMTIWLGIYAYKGLLMFLFCFLAWET	RNVSIIPALNDSKYIGMSVYNGIMCIIGA	667		
Db	710	FLTRDQPNVQFCIVALYIIFCSTITL	CLVFVKLITLRTNPDAATQNRFFQTNQKKED	769		
QY	668	FLTRDQPNVQFCIVALYIIFCSTITL	CLVFVKLITLRTNPDAATQNRFFQTNQKKED	727		
Db	770	SKTSTSVTQSVNQASTSRLEGLOS	ENHRLMKITELDKDLEEVMTQLODTEKTYIKQNH	829		
QY	728	SKTSTSVTQSVNQASTSRLEGLOS	ENHRLMKITELDKDLEEVMTQLODTEKTYIKQNH	787		
Db	830	YOELNDILNLGNFTSTDDGKAILK	NHLDQNPOLQWNTPEPSRTCKDPIEDINSPEHIOR	889		
QY	788	YOELNDILNLGNFTSTDDGKAILK	NHLDQNPOLQWNTPEPSRTCKDPIEDINSPEHIOR	847		
Db	890	RLSLQLPILHHAYLPSIGGV	DASCVPSCVPTASPRHRHVPSPFRVNVSGL	940		

QY 848 RLSQLPILHHAYLPSIGVDASCVPCVPTASPRHRHRVPPFRVMVSGL 898

RESULT 3
ID Q9Y133 PRELIMINARY; PRT: 1221 AA.
AC Q9Y133;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DE BCDA.GH07312.
DE BCDA.GH07312.
GN BCDA.GH07312.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
SEQUENCE FROM N.A.
RA RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,
RA AGBAYANI A., ARCAINA T.T., BAXTER E., BLAZEJ R.G., BUTENHOFF C.,
RA CHAMPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARFAN D.E., FRISE E.,
RA GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM J.,
RA HOUSTON K.A., HUMMASTI S.R., KIM E., LI P., MOSHREFI M., PACLEB J.M.,
RA PARK S., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T.,
RA CELNIKER S.E.;
RT "Full length Drosophila melanogaster cDNA sequence."
RL EMBL: AF145639; AAD38614.1; -;
DR EMBL: AF145639; AAD38614.1; -;
SQ SEQUENCE 1221 AA; 138124 MW; CE3B7865 CRC32;

Query Match 34.3%; Score 2253; DB 5; Length 1221;
Best Local Similarity 41.9%; Pred. No. 0.00e+00;
Matches 325; Conservative 197; Mismatches 231; Indels 22; Gaps 18;

Db 21 AC-GRKASDVYIAGFFPYGDSVNTGRVMPVSVKALGHVNECHKILANRLHMMW 79
QY 3 SCPARSAT-GPUSIMGLMPLTEKVAKGSTGRVLPVAVELAEIQHNES-LLRPFLDLRL 60
Db 80 NDTQCNAAYGVKSFDDMHSGVLMFGAACHTHYTDPIAKASKWHHTQLSYADTHPMF 139
QY 61 YTECDNAGKAFDAIKYGNHLMVFGVCPVSTIIAESLQGNLVLSFAATTPLV 120
Db 140 T-KDAPNFRVVPVSENAPRLALLKEFNWTRVGTVYQNEPRYSPLPHNHVADLDAME 198
QY 121 ADKKKYPYFERTVPSDNVAPNPAIKLLKHQYKRVGTLTQDVQRESEVRNDLTGLYGED 180
Db 199 VEWETQSFVDAESLKLREKQVRIILGNFNEHFAKACEAYKLDWYGRAYOWLMA 258
QY 181 IFISDTESEFNDPCTSVKRLKGNDRILQGDQDNMAAKVFCAYEENYKSKYQWIIIPG 240
Db 259 TYSTDWNN-V-TQ-DSE-CSVSEIATALEGAILVDLLPLSTSGDITVAGITADEYLVEYD 314
QY 241 WYEPHWEQVHTANSRCLRNLAAMEGYICVDFEPLSSKQIKTISGKTPOQYREYN 300
Db 315 RLR-GTEYSRFGHYVDGWA-A-AL--AIQYV-AEKREDDLTTHFDYRVKOWESVFLBAL 368
QY 301 NKRSGVGPCKFHYADYGIWIAKTLQRAMETLHASSRHQIQDFNYTDHTLGRILNAM 360
Db 369 RNTSPGCVTPVRYNNERKANILINQOLGOMEXIGEVSOKSHLDSLCKPVKWKCT 428
QY 361 NETNFFGVTVQVFRNGERMGTKTFQDSDREVKVGEYNAVADTLEI-INDTIRFQGE 419
Db 429 PKDRTLIVIEHSQVNTIYVSASAVIGVIAATVAFNFKYRNQVIRKSSPHLNNL 488
QY 420 PKDKTIIIEQLRKISLPLYSILSALTILGIMASAFNFNKNRKNQKILKSSPYMNL 479
Db 489 IIVGCMYTLISIFGLDITLSSVAAFYICTARAWILMAGSLSFSGAMFSKTRVHSIF 548
QY 480 IILGGLSVASIFLGLDGSFVSEKTFETLCTVRTWILTGTATGAMFAKTRVHAIF 539
Db 549 TDLKLNKKVICYQFPMVGVLLADIALITWQADPPYRTKQLPLHNEID-DVLV 607
QY 540 KNYMKKKIKDKOKLLVIGVGMILLDLICWQAVDPL-RRTEVKEYSMEPDPAGRDISI 598

Db 608 IPENEYCSQSEHMTIFVSIYAYKGLLVFGAFWETRHVSIPALNDSKHIGFSYNNVFI 667
QY 599 RPLLEHCENTHMTIWLGIYAYKGLMLFGCFLAWETRVNSIPALNDSKYIGMSYNNVGI 658
Db 668 TCLAAGAAISLVISDRKDLVFLVLSFIIFCTTATLCLVFPVKLVKRNQGVV-DKRV 726
QY 659 MCIIIGAASFLTRDQPNVQFCIVALVIFCSTITLCLVEVPKLTILRTNPDAAONRRFQ 718
Db 727 ATLPRMSKNGRRDSSVCELEQ---RLRQVKNTRCFKALMEKNELOALIRKL 777
QY 719 FTQNKQKEDSTSTSVTSVQASTSLEGLQSEHRLRMKITELDKDLBEVTMQL 773

RESULT 4
ID Q96022 PRELIMINARY; PRT: 844 AA.
AC Q96022;
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DE GABAB RECEPTOR, SUBUNIT 1B PRECURSOR.
GN GABAB-R1 OR GABA-B R1B OR GABBR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,
RA BARNES A.A., ENSON P., FOORD S.M., MARSHALL F.H.;
RT "Heterodimerisation is required to form a functional GABAB receptor."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE; 99061981;
RA KAUPMANN K., SCHULER V., MOSBACHER J., BISCHOFF S., BITTIGER H.,
RA HEID J., FROESTL W., LEONHARD S., PFAFF T., KARSCHIN A., BETTLER B.;
RT "Human gamma-aminobutyric acid type B receptors are differentially
expressed and regulate inwardly rectifying K+ channels."
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
RN [3]
SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ012186; CAA0940.1; -;
DR EMBL; AJ225029; CAA12360.1; -;
DR EMBL; AL031983; CAA21454.1; -;
KW Signal; Receptor.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 844 GABAB RECEPTOR, SUBUNIT 1B.
SQ SEQUENCE 844 AA; 95148 MW; C7342B77 CRC32;

Query Match 25.7%; Score 1687; DB 4; Length 844;
Best Local Similarity 36.2%; Pred. No. 0.00e+00;
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

Db 68 GOACQPAVEMALEDVNSRDILPDYELKLHDSKDPQATKYLYELLYNDPIKILMP 127
QY 31 GRGVLPAVELAIEQIRNE-SLLRPYFLDLRLDYDECDNAKGLKAFYDAIKYGNHLMVFG 89
Db 128 G-CSSVSTLVAEARMNVLIVSYGSSSPALSNRQRPPTFFTRTHPSLTHNPRVKLFEX 186
QY 90 GVCPSVTIIAESLQGNLVLSFAATTPLVADKKYPYFERTVPSDNVAPNPAIKLLKH 149
Db 187 WGKKIATIOOTTEVFTSTLDDLEERVKEAGIEITRQSFSDPVPVPLKQDARIIV 246
QY 150 YQWKRVTGLTQDVQRESEVRNDLTGLYGEDIEISDTESEFNDPCTSVKRLKGNDRIL 209
Db 247 GLFYETEARVCEVYKERLFGKKYVWFLIGVADNWF-KIY-DP-SINCTVDMEAVE 303
QY 210 GQFQDNMAKVFCCAYEENYKSKYQWIIIGWVEPFWHEQVHTANSRCLRNLAAME 269
Db 304 GHITTEIVMLNPANTRISNNTSQEFVEKLTIKRLKRHPETGGFGFAPLAYDAIWALALA 363


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QY 150 YQWKRVGTLTQDQRFSEVRNDLTGLVGEDIEISDTESFSNDPCTSVKXKLGNDVRIL 209
Db 247 GLFYETEARKVCEVYKERLFGKKYVWFLIGNYADNWF-KTY-DP-SINCTVEEMTEAVE 303
QY 210 GQFDQNAAKVFCCEAEEENYGSKYOWIIPGWYEPSSWEQVHTEANSSRCLKNLLAAME 269
Db 304 GHTTTEIVMLNPANTRISNMTSQBEVEKLTAKLRKHPEETGGQOEAPLAYDAIWAALA 363
QY 270 GYIGVDFEFLSSKQIKTISGKTPOQY-EREYNN-KRSGVGPSKFH-G-YAYDGIWVIART 325
Db 364 LNKTSGG--GGRSGVRLEDFNNGTITDQIYRAMNSSSFEVSGHVYFDASGRMAWTL 421
QY 326 LQAMETLHASSRHQRIQDFNTDHTLGRILNAMNEINFGVGTQGVVF-RNGERMGTIK 384
Db 422 IEQLOGGSKKIGYDSTKDDLSW-SKTDKWIGGSPPADQTLVKTFRFLSOKLFIYSV 480
QY 385 FTQFQDSREVKVGEYNADVADTLEIINDIRFQGSPPDKTIILQELKISLPLYSILSA 444
Db 481 LSSLGIVLAVCLSNFYNSHVRYIONOPNNLNTAVGCSIALAAVFPGLDGYHIGRS 540
QY 445 LTILGIMASAFLEFNKRNOKLIKMSPPYNNLIILGMLSYASIFLGLDGSFVSEK 504
Db 541 QPPEVCOARLWLLGLGFSIGSGSMETKIWWVHTVETKKEEKWKRTLEPKLYATVGLL 600
QY 505 TPETLCTVRTWLTGVYTTAFGAMFAKTRVHAIF--KNVXMK-KKIIKDKQLLVIVGGM 561
Db 601 VGMIDLTLAIQWIVDPLHRTIETFAKEPKEDIDVSIPLQLEHSCSKKMTWLGIIFYGK 660
QY 562 LLDILCILCQWAVDPLRTVEKYSMEPDPAGRDISIRPLEHCENTHMTWLTGIVYAYK 621
Db 661 GLLLLGLIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQOAAFAFA 720
QY 622 GLLMLFGCLAWETRNVSPALNDSKYIGMSVYNGVIMCIIGAASVFLTRDQPNVQFCIV 681
Db 721 SLAIVFSSYITLVLFVPMRRLITRGE 748
QY 682 ALVITFCSTITLCIVFVFKLITLRTNPD 709

RESULT 9
ID Q9WV17 PRELIMINARY; PRT; 844 AA.
AC Q9WV17;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE 573K1.1-2 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1B).
GN 573K1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078630; CAB44991.1; -.
KW Receptor.
SQ SEQUENCE 844 AA; 95022 MW; 96F2ED2A CRC32;

Query Match 25.6%; Score 1683; DB 11; Length 844;
Best Local Similarity 36.2%; Pred. No. 0.00e+00;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 68 GOACOPAVEALEVDNSRRDILPDYELKLIHDSKCDPGQATKYLVELLYNDPIKILMP 127
QY 31 GRGVLPAVEALAEIOIRNE-SLLRPYFLDLRLDYDTECDNAGLKAFDAIKYGNHMLVFG 89
Db 128 G-CSSVSTLVAEARMNWLIVLSYSSSPALSNRQFPPTFRTHPSATLHNPTRVKLEK 186
QY 90 GVCPSVTSIIAESIQGNLVQLSFAATTPVLADKKKYPYFRTVPSDNVNPAILKXK 149
Db 187 WGWKKIATIQOTTEVFTSTLDDLEERKEAGIEITFQSFSDPVPVNNLKRQDRIIV 246
QY 150 YQWKRVGTLTQDQRFSEVRNDLTGLVGEDIEISDTESFSNDPCTSVKXKLGNDVRIL 209
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Db 247 GLFYETEARKVCEVYKERLFGKKYVWFLIGNYADNWF-KTY-DP-SINCTVEEMTEAVE 303
QY 210 GQFDQNAAKVFCCEAEEENYGSKYOWIIPGWYEPSSWEQVHTEANSSRCLKNLLAAME 269
Db 304 GHTTTEIVMLNPANTRISNMTSQBEVEKLTAKLRKHPEETGGQOEAPLAYDAIWAALA 363
QY 270 GYIGVDFEFLSSKQIKTISGKTPOQY-EREYNN-KRSGVGPSKFH-G-YAYDGIWVIART 325
Db 364 LNKTSGG--GGRSGVRLEDFNNGTITDQIYRAMNSSSFEVSGHVYFDASGRMAWTL 421
QY 326 LQAMETLHASSRHQRIQDFNTDHTLGRILNAMNEINFGVGTQGVVF-RNGERMGTIK 384
Db 422 IEQLOGGSKKIGYDSTKDDLSW-SKTDKWIGGSPPADQTLVKTFRFLSOKLFIYSV 480
QY 385 FTQFQDSREVKVGEYNADVADTLEIINDIRFQGSPPDKTIILQELKISLPLYSILSA 444
Db 481 LSSLGIVLAVCLSNFYNSHVRYIONOPNNLNTAVGCSIALAAVFPGLDGYHIGRS 540
QY 445 LTILGIMASAFLEFNKRNOKLIKMSPPYNNLIILGMLSYASIFLGLDGSFVSEK 504
Db 541 QPPEVCOARLWLLGLGFSIGSGSMETKIWWVHTVETKKEEKWKRTLEPKLYATVGLL 600
QY 505 TPETLCTVRTWLTGVYTTAFGAMFAKTRVHAIF--KNVXMK-KKIIKDKQLLVIVGGM 561
Db 601 VGMIDLTLAIQWIVDPLHRTIETFAKEPKEDIDVSIPLQLEHSCSKKMTWLGIIFYGK 660
QY 562 LLDILCILCQWAVDPLRTVEKYSMEPDPAGRDISIRPLEHCENTHMTWLTGIVYAYK 621
Db 661 GLLLLGLIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQOAAFAFA 720
QY 622 GLLMLFGCLAWETRNVSPALNDSKYIGMSVYNGVIMCIIGAASVFLTRDQPNVQFCIV 681
Db 721 SLAIVFSSYITLVLFVPMRRLITRGE 748
QY 682 ALVITFCSTITLCIVFVFKLITLRTNPD 709

RESULT 10
ID Q08621 PRELIMINARY; PRT; 844 AA.
AC Q08621;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GABA-BR1B RECEPTOR.
GN GABA-BR1B OR GABABR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIF (RAI F[SPF]); TISSUE=CORTEX, AND CEREBELLUM;
RX MEDLINE: 9722131.
RA KAUPMANN K., HEGGEL K., HEID J., FLOR P.J., BISCHOFF S., MICKEL S.J.,
RA MCMASTER G., ANGST C., BITTIGER H., FROESTL W., BETTLER B.;
RT "Expression cloning of GABA(B) receptors uncovers similarity to
RT metabotropic glutamate receptors.";
RL Nature 386:239-246(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR;
RA PFAFF T., MALITSCHKE B., KAUPMANN K., BETTLER B., KARSCHIN K.;
RT "Alternative splicing generates a novel isoform of the rat
RT metabotropic GABA(B) receptor.";
RL Eur. J. Neurosci. 0:0-0(1999).
DR EMBL; Y10370; CAA71399.1; -.
DR EMBL; AF110797; AAD19657.1; -.
DR EMBL; AF110796; AAD19657.1; JOINED.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW Receptor.
SQ SEQUENCE 844 AA; 95037 MW; 6611F68D CRC32;
```


Query Match	25.6%	Score 1681;	DB 11;	Length 960;
Best Local Similarity	36.2%	Pred. No. 0.00e+00;		
Matches	249;	Conservative 177;	Mismatches 246;	Indels 16; Gaps 14;
Db	184	GQACQPAVEMALEDNSRRDILPVDYELKLHHSDCKDQCQATKYLYELLYNDPIKIILMP	243	
Qy	31	GRGVLPVELATEIQIRNE-SLLRPFYLDRLXYDTECDNAKGLKAFYDAIKYGNHLMVFG	89	
Db	244	G-CSSVSTLVAAERAMNWLIVLSYGSSSPALSNRQRFPTFFTHPSATLHNPTKLUFEK	302	
Qy	90	GVCPSVTSITAESLQGNLVLSFAATTPLADKKYFYFFFTVPSDVAVNPAIILKLKH	149	
Db	303	WGKKKIATIQOTTEVFTSTLDLEERVKEAGIEITFQSFSDPAVPYKNLKRODARIIV	362	
Qy	150	YQWRVGTUTQVQRFSVRNDLTGVLYGEDIISISTESFSNDPCTSVKKLUGNDNVILL	209	
Db	363	GLFYEAREKRVCEYKBERLFGKYVWFLGWADNWF-KTY-DP-SINCTVEEMTAEVE	419	
Qy	210	QGFDNMAAKVCCAYEENMYGSKYQWIIPGWEPYSWQVHTEANSRCLRKNLLAAE	269	
Db	420	GHTITVELMNPANTRTSINMTSOEFVEKLTKLKHPDETGGFOEAPLAYDAIWAALA	479	
Qy	270	GYIGVDPEFLSSKOJKTSGTPOQY-EREYNN-KRSYGVPSKFFH-G-YAYDGIWIAKT	325	
Db	480	LNKTSGC--GGRSGVRLDEFNVMNOTITDOIYRAMNSSFEQVGHGVYFDAGSGRMAWTL	537	
Qy	326	LQARETLHASSRHORIQDFNYDHTLGRILLNAMNETFFGVGTQGVF-RNGERMGTIK	384	
Db	538	IEQLOGYSKKIGYDSTKDDLW-SKTDKWIJGSSPPAQDTLVIKTFRFLSQKLFISVSV	596	

Query Match	20.6%	Score	1352	DB 11	Length	662			
Best Local Similarity	34.6%	Pred. No.	3.12e-255						
Matches	207	Conservative	156	Mismatches	220	Indels	16	Gaps	14

Db	68	GOACOPAVEMALEIDVNSRRDILPDYELKLIHDSKDCPQOATKYLYELLYNDPIKIILMP	127
QY	31	GRGVLPVLAELAIEQIRNE-SILLRPYFLDLRLYDTECDNAKGLKAFDAIKYGNPHLWVFG	89
Db	128	G-CSSVSTVLAEARMMNLIVLYSGSSPALSNRORFPFFFTFTHPSATLHNPTVKLFEK	186
QY	90	GVCPSVTSIIAESLQGNLWOLSEFAATTPVLADKKKYFYFTVPSDNAVNPAILKLLKH	149
Db	187	WQKKLIATIQOTTEVFTSTLDDLEERKEAGTEITFROSFDSPDPAVPVKLNKRDARIIV	246
QY	150	YQWKRVGHITQDVRQFSEVRNDITGVLYGEDTEISDTSEFSNDPCTSVKKLKGNDVRILL	209
Db	247	GLFYETEARKEVCEYKERLFGKKYVWFLGMYADNWF-KTY-DP-SINCTVEEMTEAVE	303
QY	210	GQFDQNMAAKFCCEAYENMYGKYQWIIIPGWYFESWVEQVHTEANSRCLURKLLAAE	269
Db	304	GHTTETVWLNPANTRISNWTQSEFVEKLTRELKXHPDETGGQEPALDAYDAWALALA	363
QY	270	GYIGVDFEPLSKQIKTISGKTPOQY-EREYNN-KRSGVGPSKFH-G-YA'DGIGWIAKT	325
Db	364	LAKTSGG--GGRSGVRLEDENNYNNQITQDQIVRAMNSSFEGVGHVYVFDAGSRMAWTL	421
QY	326	LQAMETLHASRRHQIODENYTDHILGRILLNAMNEINFQVGTQGVVF-RNGERMGITK	384
Db	422	IEOLOGGSYKKIIGYYDTKDDLSW-SKTDKWIIGSGPPADQTLVTKTFEFLSQKLFIISVSV	480
QY	385	FTFODSREVKYGEYNAVADTLEIINDTRFQSESPPKDKTIIELQRLKISUPYLSILA	444

(TM)

Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	241	3.7	908	MGR8_MOUSE	METABOTROPIC GLUTAMATE	1.92e-21
2	236	3.6	871	MGR6_RAT	METABOTROPIC GLUTAMATE	1.52e-20
3	237	3.6	908	MGR8_RAT	METABOTROPIC GLUTAMATE	1.01e-20
4	232	3.5	908	MGR8_HUMAN	METABOTROPIC GLUTAMATE	7.93e-20
5	228	3.5	912	MGR4_HUMAN	METABOTROPIC GLUTAMATE	4.09e-19
6	225	3.4	877	MGR6_HUMAN	METABOTROPIC GLUTAMATE	1.39e-18
7	225	3.4	912	MGR4_RAT	METABOTROPIC GLUTAMATE	1.39e-18
8	214	3.3	915	MGR7_RAT	METABOTROPIC GLUTAMATE	1.19e-16
9	214	3.3	915	MGR7_HUMAN	METABOTROPIC GLUTAMATE	1.19e-16
10	215	3.3	1203	MGR5_RAT	METABOTROPIC GLUTAMATE	7.94e-17
11	215	3.3	1212	MGR5_HUMAN	METABOTROPIC GLUTAMATE	7.94e-17
12	205	3.1	976	MGR_DROME	METABOTROPIC GLUTAMATE	4.26e-15
13	196	3.0	872	MGR2_HUMAN	METABOTROPIC GLUTAMATE	1.45e-13
14	189	2.9	872	MGR2_RAT	METABOTROPIC GLUTAMATE	2.17e-12
15	189	2.9	1079	CASR_RAT	EXTRACELLULAR CALCIUM	2.17e-12
16	187	2.8	877	CASR3_HUMAN	METABOTROPIC GLUTAMATE	4.56e-12
17	187	2.8	879	MGR3_RAT	METABOTROPIC GLUTAMATE	4.56e-12
18	184	2.8	1078	CASR_HUMAN	EXTRACELLULAR CALCIUM	1.46e-11
19	182	2.8	1085	CASR_BOVIN	EXTRACELLULAR CALCIUM	3.11e-11
20	186	2.8	1194	MGR1_HUMAN	METABOTROPIC GLUTAMATE	6.82e-12
21	186	2.8	1199	MGR1_RAT	METABOTROPIC GLUTAMATE	6.82e-12
22	166	2.5	986	CYGR_ARBPB	RESACT RECEPTOR PRECUR	1.17e-08
23	167	2.5	1108	CYGF_RAT	RETINAL GUANYLYL GCLA	8.14e-09


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AC DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR MGLUR8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97168760.
RA SAUGHSTAD J.A., KINZIE J.M., SHINOHARA M.M., SEGERSON T.P.,
RA WESTBROOK G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile.";
RL Mol. Pharmacol. 51:119-125(1997).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION INCEREBRAL CORTEX,
CC HIPPOCAMPUS, CEREBELLUM, AND MAMMILLARY BODY.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; GCR_1411; -.
DR GCRDB; GCR_1411; -.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
SQ SEQUENCE 908 AA; 101866 MW; 5043ff81 CRC32;

```

Query Match 3.6%; Score 237; DB 1; Length 908;
 Best Local Similarity 22.3%; Pred No. 1,01e-20;
 Matches 63; Conservative 96; Mismatches 100; Indels 24; Gaps 21;

DB 590 IAILGII-ATTFTVIVFVRYNDTPVRASGRSLSVLLTGIFLCYSITFLM-I-AA--PD 644

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OY 445 LTILGIMASAFLEFN-IKRNQKLIKMSPPYMNLIILGMLSYASIFLFGDGSFVSE 503
DB 645 -TI--ICSFRIFLGLGCFSYAALLTKTHRIHRIPEQKSKVTPAKFISPAQSLVITES 701
OY 504 KTFETLCTVTRTWILTVGTTFAGFAMFAKTRVWHAIFKNVKK-K--KIIKDOKLLVIVGG 560
DB 702 LISVQLLGCVFVVDVDP-PHTIIDYG-EQRTLDPE-NARGVLK-CDISDLSL-ICSL-GY 755
OY 561 MLLIDLCLICQAVDPLRRTVEKYSMEPPDAGRDSIRPLEHCENTHMTIWLGIYVAY 620
DB 756 SILLMV-TC-TVYAIKTRGVPEPTEAKPGFTWYTCIIWLAFIPFPGTAQSAEKMYI 813
OY 621 KGLLMFGCFLAWETRNVSIP-ALNDSKYIGMSVYNYGIMCIIGAAVSFLTRQPNVOFC 679
DB 814 QTTTLTVSMISLASVSLGMLYMPKVIYIIIFHPQNVOKKRKF 856
OY 680 -IVALVI-I-FCSITILCLVFPVKLIILRTNPDAATONRRFOF 719
RESULT 4
ID MGR8_HUMAN STANDARD; PRT; 908 AA.
AC O00222; O15493;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR MGLUR8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98141892.
RA WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
RA ROSTECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELAGAJE R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97446143.
RA SCHERER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.;
RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
RT disproportionately large gene located at 7q31.3-q32.1.";
Genomics 44:232-236(1997).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U92459; AAB51764.1; -.
DR EMBL; U95025; AAB72040.1; -.
DR GCRDB; GCR_1889; -.
DR GCRDB; GCR_2604; -.
DR MIM; 601116; -.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.

```

```
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR. 8.
FT DOMAIN 34 593 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CONFLICT 565 565 R -> A (IN REF. 2).
FT CONFLICT 194 194 T -> I (IN REF. 2).
FT CONFLICT 460 460 A -> G (IN REF. 2).
FT CONFLICT 642 642 N -> I (IN REF. 2).
FT CONFLICT 768 768 S -> T (IN REF. 2).
FT CONFLICT 904 904
SQ SEQUENCE 908 AA; 101741 MW; 188650F CRC32;

Query Match 3.5%; Score 232; DB 1; Length 908;
Best Local Similarity 23.0%; Pred No. 7.93e-20;
Matches 65; Conservative 96; Mismatches 98; Indels 24; Gaps 21;

Db 590 VAILGII-ATTEFVIVTFVRYNDTPIVRASGRELVSLLTGIFLCYSITFLM-I-AA--PD 644
QY 445 LTIILGIMASAFLEN-IKRNOKLIKSSPYMNNLIILGCMLSYASIFLGLDGSFVSE 503

Db 645 -TI--ICSFRRVFLGLGMCFSYALLTTNRIHRIPEOGKKSVTAPKFIASPASOLVTFIS 701
QY 504 KTFELCTVTRWILVGYTTAFGAMFAKTRVHAIFKNVKK-K-KIIOKQLLVIVGG 560

Db 702 LISVOLLGVFVWVDDPHIID-YG-EQRTLDPEKA-RGVLK-CDISLDSL-ICSL-GY 755
QY 561 MLILDLICILICQWADPLRRIVERKYSMEPDAGRDISRPLEHCENHTMTWIGVIYAY 620

Db 756 SILLMV-TCTVYANKTRGPV-ETFEAKPIGFTMYTTCIIWLAFIPFFGTAQSAEKWYI 813
QY 621 KGLLMFGCEL-AWETRVNSIPALNDSKYIGMSVYNYGIMCIIGAAVSFLTRDQPNVQFC 679

Db 814 QTTILTVSNLSASVSLGMLYMPKVYIIIFHPQONVOKRRKSF 856
QY 680 -IVALVI-I-FCSTITLCLVFPVKLITLRTNPDAATQNRRFQF 719

RESULT 5
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MAKOFF A., LELCHUK R., OXER M., HARRINGTON K., EMSON P.;
RT "Molecular characterization and localization of human metabotropic
glutamate receptor type 4."
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
```

Query Match

3.5%; Score 228; DB 1; Length 912;

```
RN [2]
RX SEQUENCE FROM N.A.
RP MEDLINE; 98141892.
RA WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
RA ROSTECK P.R. JR., JOHNSON B.G., SCHORPP D.D., BELAGAJE R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and pharmacological
RT pharmacological properties in RGT cells."
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95342351.
RA FLOR P.J., LUKIC S., RUEGG D., LEONHARDT T., KNOEPFEL T., KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 4."
RL Neuropharmacology 34:149-155(1995).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST. TO MGLUR6.
CC -----
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CC -----
DR EMBL; X80818; CAA56784.1; -
DR EMBL; U92457; AAB51762.1; -
DR GCRDB; GCR_1891; -
DR GCRDB; GCR_2069; -
DR MIM; 604100; -
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32
FT CHAIN 33 912
FT DOMAIN 33 587 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT TRANSMEM 588 610 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 611 624 I (POTENTIAL).
FT TRANSMEM 625 645 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 646 656 II (POTENTIAL).
FT TRANSMEM 657 675 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 676 699 III (POTENTIAL).
FT TRANSMEM 700 720 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 721 750 IV (POTENTIAL).
FT TRANSMEM 751 772 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 773 785 V (POTENTIAL).
FT TRANSMEM 786 808 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 809 821 VI (POTENTIAL).
FT TRANSMEM 822 847 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 848 912 VII (POTENTIAL).
FT CARBOHYD 98 98 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 301 301 POTENTIAL.
FT CARBOHYD 454 454 POTENTIAL.
FT CARBOHYD 484 484 POTENTIAL.
FT CARBOHYD 569 569 POTENTIAL.
SQ SEQUENCE 912 AA; 101867 MW; 740D9054 CRC32;
```


DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGLUR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RC MEDLINE; 92317054.
RA ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;
RT "Molecular characterization of a novel metabotropic glutamate
RT receptor mGluR5 coupled to inositol phosphate/Ca2+ signal
RT transduction.";
RT J. Biol. Chem. 267:13361-13368(1992).
RN [2]
RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=BRAIN;
RC MEDLINE; 93343913.
RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon.";
RT Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
CC CENTRAL NERVOUS SYSTEM.
CC -!- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE >
CC TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR1.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; D10891; -; NOT_ANNOTATED_CDS.
DR EMBL; S64315; AAB27666.1; -;
DR PIR; A42916; A42916.
DR GCRDB; GCR_0444; -;
DR GCRDB; GCR_0760; -;
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1203 METABOTROPIC GLUTAMATE RECEPTOR 5.
FT DOMAIN 22 578 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 579 601 I (POTENTIAL).
FT DOMAIN 602 615 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 616 636 II (POTENTIAL).
FT DOMAIN 637 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 666 III (POTENTIAL).
FT DOMAIN 667 692 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 693 713 IV (POTENTIAL).
FT DOMAIN 714 736 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 737 758 V (POTENTIAL).
FT DOMAIN 759 771 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 772 794 VI (POTENTIAL).
FT DOMAIN 795 800 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 801 826 VII (POTENTIAL).

FT DOMAIN 827 1203 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 88 POTENTIAL.
FT CARBOHYD 209 209 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 381 381 POTENTIAL.
FT CARBOHYD 444 444 POTENTIAL.
FT CARBOHYD 733 733 POTENTIAL.
FT VARSPLIC 876 907 MISSING (IN ISOFORM 5A).
SQ SEQUENCE 1203 AA; 131885 MW; 2955EA33 CRC32;
Query Match 3.3%; Score 215; DB 1; Length 1203;
Best Local Similarity 28.3%; Pred. No. 7.94e-17;
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;
Db 655 AMSYSALVTKTNRIRILAGSK-KKICTKPRFMSACA-QLVIAF-ILIC---IQ-LGII 707
QY 522 TTAFAEMFAKTWRVHAIFKNVKKKKIIDKQLLVIVGMLLIDLCILICWQAVDPLRT 581
Db 708 VALFMEPPDIDMHDYPSREVLYICNTNLGV-VTPL-GYNGLLIL-SCTFYAFKTRNP 764
QY 582 VEKYSMEPPDAGRDI-SIRPLLEHCENTHMTIWLGIYVAYKGLLMFGC-FLAWETRNVS 639
Db 765 -ANFNEAKVIAFTMTTCTIILAFVPI-YFGSNYKIIIMCF-S-VSL-SATVALGCM-FV 818
QY 640 IPALNDSKTIIGMSVNVGIMCIIGAASFLTRDQPNVQFCIVALVIFCSTITL-CLIVFV 698
Db 819 PKVYIILAKPE 829
QY 699 PKLITLRTNPD 709
RESULT 11
ID MGR5_HUMAN STANDARD; PRT; 1212 AA.
AC P41594;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGLUR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RC MEDLINE; 94197696.
RA MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;
RT "Molecular cloning and the functional expression of two isoforms of
RT human metabotropic glutamate receptor subtype 5.";
RL Biochem. Biophys. Res. Commun. 199:1136-1143(1994).
RN [2]
RP REVISIONS.
RA KATSUKI F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 860-952 FROM N.A.
RC TISSUE=BRAIN;
RC MEDLINE; 93343913.
RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon.";
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR1.


```
Db 681 AL-----IAKPTIG-CVLRFGVGFSIIYSALTNTKNTNRISIFHSASKSAQRLKYISP 735
QY 495 GLDGSFVSEKTELTCTVTRTWLTGYTTAFGAMFAKTRVHAIFKNV-K-MKK-KIKD 551
Db 736 QSOVVITSLIAQVLIMVMVPEP-PGT--RFYI-PDR--REV-I---LK-CKIDMS 784
QY 552 QKLIVGVGMLLDICILICQWAVDPLRTVEKYSMEPDPAGRDISRPLEHCENTHMT 611
Db 785 FIFSOLYN-MILITICTIYAI-KTRKIP-ENFNESKFIGFTMYTTCIIWLAFAPYRGTG 841
QY 612 IWLGIYAYKGLMLFGCLFLAWETRNVSPALNDSKYIGMSVYVNGIMCIIGAAYSFLTR 671
Db 842 NSYEVQTTLCISLSASVALVCL-YSPKVIYLVFHPD 879
QY 672 DQPNVQFCIVALVIFCSTITL-CLVFPVKLTITLTNP 709

RESULT 13
ID MGR2_HUMAN STANDARD; PRT; 872 AA.
AC Q14416;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GN GRM2 OR MGLUR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 95346007.
RA FLOR P.J., LINDAUER K., PUTTNER I., RUEGG D., LUKIC S., KNOPFEL T.,
RA KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 2.";
RL Eur. J. Neurosci. 7:622-629(1995).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE
CC ADULT BRAIN AS WELL AS IN FETAL BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR3.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L35318; AAA76855.1; -
DR GCRDB: GCR_1846; -
DR MIN: 604099; -
DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 872 METABOTROPIC GLUTAMATE RECEPTOR 2.
FT DOMAIN 19 567 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 568 590 I (POTENTIAL).
FT DOMAIN 591 604 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 605 625 II (POTENTIAL).
FT DOMAIN 626 636 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 637 655
FT DOMAIN 656 679
FT TRANSMEM 680 700
FT DOMAIN 701 725
FT TRANSMEM 726 747
FT DOMAIN 748 760
FT TRANSMEM 761 783
FT DOMAIN 784 793
FT TRANSMEM 794 819
FT DOMAIN 820 872
FT CARBOHYD 203 203
FT CARBOHYD 286 286
FT CARBOHYD 338 338
FT CARBOHYD 402 402
FT CARBOHYD 547 547
SQ SEQUENCE 872 AA; 95507 MW; 9369084C CRC32;

Query Match 3.0%; Score 196; DB 1; Length 872;
Best Local Similarity 24.7%; Pred. No. 1.45e-13;
Matches 55; Conservative 68; Mismatches 78; Indels 22; Gaps 19;

Db 611 GGVFLCYCMTFIFIA-KPSTAVCTLRRLGLGTAFSCVYSALLTNTNRIFPGAREGAQ 669
QY 489 ASIFL-FGLDGSFVSEKTFETLCTVTRTWLTGYTTAFGAMFAKTRVHAIFKNV-K-MK 545
Db 670 RPRFISPAQVAICLALISGQLLIWVAVLVEA-PGT-GK-ETAPER--REV-V-TL--R 720
QY 546 K-KIKDQKLLVIVGMLLDICILICQWAVDPLRTVEKYSMEPDPAGRDISRPLEH 604
Db 721 CNHRDASM-LGSL-AYNVLLIAL-CTLYAFNTRKCP-ENFNKAEFIGFTMYTTCIIWLAL 776
QY 605 CENTHMTLGIYAYKGLMLFGCLF-AWETRNVSIPALNDSKYIGMSVYVNGIMCIIG 663
Db 777 LPFVVTSSDYRVQTTMCVSVLSGSLVGLCL-FAPKLHIL 818
QY 664 AAVSFTRDQPNVQFCIVALVIFCSTITL-CLVFPVKLTITL 704

RESULT 14
ID MGR2_RAT STANDARD; PRT; 872 AA.
AC P31421;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GN GRM2 OR MGLUR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RN SEQUENCE FROM N.A.
RX TISSUE-BRAIN.
RX MEDLINE: 921110002.
RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
RA "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-173(1992).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
CC EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME
CC PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR3.
CC -----
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```

```
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CC -----
CC EMBL: M92075; -; NOT_ANNOTATED_CDS.
CC PIR: JH0561; JH0561.
CC DR HSP; P06612; IECL.
CC DR GCRDB; GCR_0361; -.
CC DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; 1.
CC DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; 1.
CC DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; 1.
CC DR PFAM; PF00003; 7tm_3; 1.
CC DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 872 METABOTROPIC GLUTAMATE RECEPTOR 2.
FT DOMAIN 19 567 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 568 590 I (POTENTIAL).
FT DOMAIN 591 604 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 605 625 II (POTENTIAL).
FT DOMAIN 626 636 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 637 655 III (POTENTIAL).
FT DOMAIN 656 679 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 680 700 IV (POTENTIAL).
FT DOMAIN 701 725 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 726 747 V (POTENTIAL).
FT DOMAIN 748 760 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 761 783 VI (POTENTIAL).
FT DOMAIN 784 793 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 794 819 VII (POTENTIAL).
FT DOMAIN 820 872 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 203 203 POTENTIAL.
FT CARBOHYD 286 286 POTENTIAL.
FT CARBOHYD 338 338 POTENTIAL.
FT CARBOHYD 402 402 POTENTIAL.
FT CARBOHYD 547 547 POTENTIAL.
SQ SEQUENCE 872 AA; 95773 MW; C3C3467E CRC32;

Query Match 2.9%; Score 189; DB 1; Length 872;
Best Local Similarity 24.7%; Pred. No. 2.17e-12;
Matches 55; Conservative 56; Mismatches 80; Indels 22; Gaps 19;

Db 611 GGVLFCYCMVFVFA-KPSTAVCTLRRLGLGTAFSCVYCALLTKNTRIARIFGARGAQ 669
Qy 489 ASIFL-FGLDGSFVSEKFTETLCIVRTWILVGYTAFGAMFAKTRVHAIFKNVK--MK 545
Db 670 RPRESPASVAICLALISGOLLIVAWLVVEA-PGR-GK-ETAPER--REV-V-TL--R 720
Qy 546 K-KIIOKQLVIVGGMLLIDLCICWQAVDPLRRVTERYSMEPDAGRDISIRPLEH 604
Db 721 CNHRDASM-LGSL-AYNVLIAL-CTLYAFKTRKCP-ENFENAKFIFGTMYTTTCIIWLAF 776
Qy 605 CENTHMTWLGIVVAYKGLLMFLGCLF-AWETRVNISPALNDSKYIGMSVYVNGVINGCIIG 663
Db 777 LPFVVTSSDRVQVTTMCVSVLSGSGVVLGCL-FAPKLHIIL 818
Qy 664 AAVSFLTRDQNPVQPCIVALVIFGCTITL-CLVFEVPKL-ITL 704

RESULT 15
ID CASR_RAT STANDARD; PRT; 1079 AA.
AC P48442;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
DE CELL CALCIUM-SENSING RECEPTOR).
OS CASR OR PCAR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY OUTER MEDULLA;

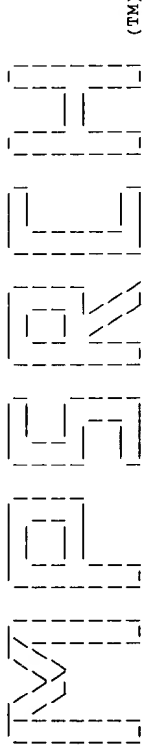
RX MEDLINE; 95116508.
RA RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E.M., HEBERT S.C.;
RT "Cloning and functional expression of a rat kidney extracellular
RT calcium/polyvalent cation-sensing receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
RN [2]
RP SEQUENCE OF 1-294 FROM N.A.
RC STRAIN-WISTAR;
RX MEDLINE; 95241465.
RA RUAT M., SNOWMAN A.M., SNYDER S.H.;
RT "Calcium sensing receptor: molecular cloning in rat and localization
RT to nerve terminals.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
CC -!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10354; AAC52149.1; -.
CC DR EMBL; U20489; AAC52195.1; -.
CC DR GCRDB; GCR_1449; -.
CC DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; 1.
CC DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; 1.
CC DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; 1.
CC DR PFAM; PF00003; 7tm_3; 1.
CC DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1079 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
FT DOMAIN 20 612 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 613 635 I (POTENTIAL).
FT DOMAIN 638 649 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 650 670 II (POTENTIAL).
FT DOMAIN 671 681 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 682 700 III (POTENTIAL).
FT DOMAIN 701 724 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 725 745 IV (POTENTIAL).
FT DOMAIN 746 769 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 770 792 V (POTENTIAL).
FT DOMAIN 793 805 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 806 828 VI (POTENTIAL).
FT DOMAIN 829 836 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 837 862 VII (POTENTIAL).
FT DOMAIN 863 1079 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 90 90 POTENTIAL.
FT CARBOHYD 130 130 POTENTIAL.
FT CARBOHYD 261 261 POTENTIAL.
FT CARBOHYD 287 287 POTENTIAL.
FT CARBOHYD 386 386 POTENTIAL.
FT CARBOHYD 446 446 POTENTIAL.
FT CARBOHYD 468 468 POTENTIAL.
FT CARBOHYD 488 488 POTENTIAL.
FT CARBOHYD 541 541 POTENTIAL.
FT CARBOHYD 594 594 POTENTIAL.
SQ SEQUENCE 1079 AA; 120867 MW; 34118BE9 CRC32;

Query Match 2.9%; Score 189; DB 1; Length 1079;
Best Local Similarity 27.5%; Pred. No. 2.17e-12;
Matches 25; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

Db 125 LDFCNCSHIPSTIAVVGATGSGVSTAVANLLGLFIYPOVSVASSRLLSNKNQKSL 184
Qy 71 LKAFYDAIKYGNHLMVFGVCPVSTIIAESLQGNLVOLSFAATTPVLADKKKPYPF 130
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Db 185 RTIPNDEHQATAMADIIIEYFRNWNVGTIAAD 215
QY 131 RTVPNDNAVNPAILKLLKHYQWKRYGTLTQD 161

Search completed: Wed Mar 15 21:27:21 2000
Job time : 398 secs.



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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Mar 15 21:09:20 2000; MasPar time 61.49 Seconds
688.883 Million cell updates/sec
Tabular output not generated.

Title: >US-09-211-755-2
Description: (1-898) from US09211755.pep
Perfect Score: 6573
Sequence: 1 MPSCPARSATGPLSLIMGLMP.....TASPRHRHVPPSRVMVSGL 898

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir62
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 55.042; Variance 120.918; scale 0.455

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1669	25.4	960	2	JE0356 gamma-aminobutyric ac	4.42e-280
2	241	3.7	908	2	I49142 metabotropic glutamat	6.66e-18
3	236	3.6	871	2	A46742 metabotropic glutamat	3.94e-17
4	225	3.4	912	2	I58149 metabotropic glutamat	1.89e-15
5	225	3.4	912	2	JH0563 metabotropic glutamat	1.89e-15
6	214	3.3	915	2	A49874 metabotropic glutamat	8.61e-14
7	215	3.3	1171	2	A42916 metabotropic glutamat	6.10e-14
8	215	3.3	1180	2	JC2132 metabotropic glutamat	6.10e-14
9	215	3.3	1212	2	JC2131 metabotropic glutamat	6.10e-14
10	189	2.9	872	2	JE0561 metabotropic glutamat	3.96e-10
11	193	2.9	940	2	T02740 hypothetical protein	1.05e-10
12	189	2.9	1079	2	I59362 calcium/polyvalent ca	3.96e-10
13	188	2.9	1218	2	S71376 glutamate receptor ho	5.51e-10
14	187	2.8	879	2	JH0562 metabotropic glutamat	7.66e-10
15	187	2.8	1078	2	S49341 calcium-sensing recep	7.66e-10
16	184	2.8	1078	2	A56715 calcium receptor (clo	2.05e-09
17	182	2.8	1085	2	S40476 Ca(2+)-sensing recept	3.93e-09
18	184	2.8	1088	2	S56715 calcium receptor (clo	2.05e-09
19	186	2.8	1199	2	A41939 G protein-coupled glu	1.06e-09
20	177	2.7	898	2	T05099 hypothetical protein	1.98e-08
21	166	2.5	986	1	OVURGA speract receptor prec	6.49e-07
22	167	2.5	1108	2	B55915 guanylate cyclase (EC	4.74e-07
23	163	2.5	1525	1	A56699 guanylate cyclase (EC	1.65e-06

24	159	2.4	1125	1	OYURCP speract receptor prec	5.68e-06
25	152	2.3	373	2	A36125 branched-chain amino	4.76e-05
26	142	2.2	1005	2	S33525 guanylate cyclase (EC	9.10e-04
27	137	2.1	535	2	A54155 natriuretic peptide r	3.82e-03
28	139	2.1	536	2	S71332 natriuretic peptide c	2.16e-03
29	136	2.1	536	2	A45409 atrial natriuretic pe	5.07e-03
30	136	2.1	537	1	A28111 natriuretic peptide r	5.07e-03
31	135	2.1	958	2	T02741 hypothetical protein	6.72e-03
32	137	2.1	1679	2	T15968 conserved hypothetica	3.82e-03
33	134	2.0	430	2	H69955 natriuretic peptide r	2.05e-02
34	131	2.0	540	1	OYHUCR hypothetical protein	8.90e-03
35	134	2.0	938	2	T01809 guanylate cyclase (EC	1.55e-02
36	132	2.0	1108	2	I59385 guanylate cyclase (EC	8.90e-03
37	134	2.0	637	2	C65129 hypothetical ABC tran	4.67e-02
38	128	1.9	676	2	S00084 myosin heavy chain, f	8.03e-02
39	126	1.9	885	2	JN0339 N-methyl-D-aspartate	8.03e-02
40	126	1.9	901	2	JN0337 N-methyl-D-aspartate	8.03e-02
41	126	1.9	922	2	JN0338 N-methyl-D-aspartate	8.03e-02
42	126	1.9	938	2	A46612 N-methyl-D-aspartate	6.13e-02
43	127	1.9	938	2	S21104 N-methyl-D-aspartate	6.13e-02
44	127	1.9	938	2	S19710 N-methyl-D-aspartate	8.03e-02
45	126	1.9	938	2	S19710 N-methyl-D-aspartate	8.03e-02

ALIGNMENTS

RESULT 1
ENTRY JE0356 #type complete
TITLE gamma-aminobutyric acid receptor B precursor - human
ALTERNATE_NAMES GABA(B) receptor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 12-Feb-1999
ACCESSIONS JE0356
REFERENCE JE0356
#authors Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante, L.; Gasparini, P.
#journal Biochem. Biophys. Res. Commun. (1998) 250:240-245
#title GABA (gamma-amino-butyric acid) neurotransmission: Identification and fine mapping of the human GABAB receptor gene
#cross-references MUID:98440782
#accession JE0356
#molecule_type mRNA
#residues 1-960 #label GRI
#cross-references GB:Y11044; NID:G2826760
#note this ORF is not annotated in GenBank entry HSGTHLAL, release 109

GENETICS
#map_position 6p21.3-6p21.3
KEYWORDS glycoprotein; neurotransmitter receptor; transmembrane protein
FEATURE
1-11 #domain signal sequence #status predicted #label SIG\
12-960 #product gamma-aminobutyric acid receptor B #status predicted #label MAT\
590-613 #domain transmembrane #status predicted #label TM1\
627-654 #domain transmembrane #status predicted #label TM2\
666-687 #domain transmembrane #status predicted #label TM3\
709-730 #domain transmembrane #status predicted #label TM4\
767-788 #domain transmembrane #status predicted #label TM5\
803-825 #domain transmembrane #status predicted #label TM6\
831-856 #domain transmembrane #status predicted #label TM7\
23,83,439,481,501, #binding_site carbohydrate (Asn) (covalent) #status predicted
513,630 #length 960 #molecular-weight 108148 #checksum 3766

SUMMARY
Query Match 25.4%; Score 1669; DB 2; Length 960;
Best Local Similarity 36.2%; Pred. No. 4.42e-280;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

DB 184 GOACOPAVEMALEDVNSRRDILPDYELKLIHHDSKDCPGQATKYLYELLYNDPIKILMP 243


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#title
Cloning and expression of a new member of the
L-2-amino-4-phosphonobutyric acid-sensitive class of
metabotropic glutamate receptors.
#cross-references MUID:94195260
#accession I57954
#status preliminary; translated from GB/EMBL/DBD
#molecule_type mRNA
#residues 1-915 #label RE2
#cross-references EMBL:008632; NID:9459657; PIDN:AAA20655.1;
PID:9459658

GENETICS
#gene MGLUR7
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS neurotransmitter receptor
SUMMARY #length 915 #molecular-weight 102231 #checksum 1873

Query Match 3.3%; Score 214; DB 2; Length 915;
Best Local Similarity 22.9%; Pred. No. 8.61e-14;
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

Db 597 LAMLGII-ATIFVWATFIRYNDPIVRASGRELSYLLTGIFLCY--IITP-L---MIA- 648
QY 445 LTIIGMIMASAFNFN-IKNRNKLKMSPPYMNIIILGGMLSYASIEFLGIDGSFVSE 503
Db 649 KPDVAVCSFRVFLGCMCISYAALTKTNRIYRIFEQKSKVTAPRLISPTSQLAITSS 708
QY 504 KTFETLCTVETWLTGVYTTAFGAMFAKTRVHAIFKNVMK-K-KLIKDKLLVIVGG 560
Db 709 LIISVQLGVI-NFGVDPNIIID-YD-EHKTMNPQA-RGVLK-CDITDLQI-ICSL-G 761
QY 561 MLLTIDL-CILICQWADVPLRTVEKYSMEPDPAGRDISIRPLEHCENTHMTWILGIYVA 619
Db 762 YSILLMW-TC-TYVAKTRGVNENFNAKPIGTMTTCIVWLAFIPFGFAQSAEKLY 819
QY 620 YKGLMLFGCFLAWERNVSIIPA-LNDSYIGMSVYNGVIMCIIGAASVFLTRDQPNVQF 678
Db 820 IQTTTLTISNLSASVALGMLPKVYIIFHPELNVOKRKRSF 863
QY 679 C-IVALVI-I-FCSTITGLVFVPKLIITLTNPDAATQNRQF 719

RESULT 7
ENTRY A42916 #type complete
TITLE metabotropic glutamate receptor mGluR5 - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
29-Jan-1999
ACCESSIONS A42916
REFERENCE #authors Nakanishi, S.; Nawa, H.; Shigemoto, R.; Mizuno, N.;
Abe, T.; Sugihara, H.
#journal J. Biol. Chem. (1992) 267:13361-13368
#title Molecular characterization of a novel metabotropic glutamate
receptor mGluR5 coupled to inositol phosphate/Ca2+ signal
transduction.
#cross-references MUID:92317054
#accession A42916
#status preliminary
#molecule_type mRNA
#residues 1-1171 #label ABE
#cross-references GB:D10891; NID:g220813; PID:d1002186; PID:g220814
#experimental_source brain
#note sequence extracted from NCBI backbone (NCBIN:107749,
NCBIP:107750)
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 1171 #molecular-weight 128289 #checksum 8594

Query Match 3.3%; Score 215; DB 2; Length 1171;
Best Local Similarity 28.3%; Pred. No. 6.10e-14;
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;

Db 655 AMSYSALVTNRIARILAGSK-KKICTKPRFMSACA-OLVIAF-ILIC---IQ-LGII 707
QY 655 AMSYSALVTNRIARILAGSK-KKICTKPRFMSACA-OLVIAF-ILIC---IQ-LGII 707
#experimental_source brain
#note sequence extracted from NCBI backbone (NCBIN:107749,
NCBIP:107750)
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 1171 #molecular-weight 128289 #checksum 8594

Query Match 3.3%; Score 215; DB 2; Length 1180;
Best Local Similarity 28.3%; Pred. No. 6.10e-14;
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;

Db 656 AMSYSALVTNRIARILAGSK-KKICTKPRFMSACA-OLVIAF-ILIC---IQ-LGII 708
QY 522 TTAFGAMFAKTRVHAIFKNVMKKIIKDQKLLYIVGGMLLIDICILICQWADVPLRT 581
Db 709 VALFIMEPDDIMHDYPSIREVYLICNTNLGV-VTPL-GYNGLLIL-SCTFYAFKTRNP 765
QY 582 VEKYSMEPDPAGRDI-SIRPLEHCENTHMTWILGIYVAYKGLMLFGC-FLAWETRNV 639
Db 766 -ANFNEAKVIAFTMTTCIILWAFVPI-YFGSNYKIITMCF-S-VSL-SATVALGCM-FV 819
QY 640 IPALNDSKYIGMSVYNGVIMCIIGAASVFLTRDQPNVQFCIIVALVIIFCSTITL-CLV 698
Db 820 PKVYIILAKPE 830
QY 699 PKLITLRTNPD 709

RESULT 9
ENTRY JC2131 #type complete
TITLE metabotropic glutamate receptor 5 B - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
05-Jan-1996

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QY 522 TTAFGAMFAKTRVHAIFKNVMKKIIKDQKLLYIVGGMLLIDICILICQWADVPLRT 581
Db 708 VALFIMEPDDIMHDYPSIREVYLICNTNLGV-VTPL-GYNGLLIL-SCTFYAFKTRNP 764
QY 582 VEKYSMEPDPAGRDI-SIRPLEHCENTHMTWILGIYVAYKGLMLFGC-FLAWETRNV 639
Db 765 -ANFNEAKVIAFTMTTCIILWAFVPI-YFGSNYKIITMCF-S-VSL-SATVALGCM-FV 818
QY 640 IPALNDSKYIGMSVYNGVIMCIIGAASVFLTRDQPNVQFCIIVALVIIFCSTITL-CLV 698
Db 819 PKVYIILAKPE 829
QY 699 PKLITLRTNPD 709

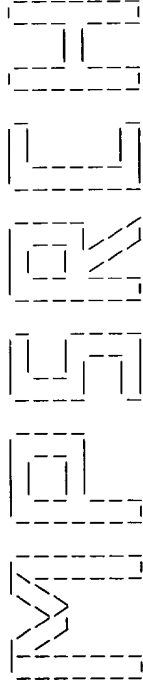
RESULT 8
ENTRY JC2132 #type complete
TITLE metabotropic glutamate receptor 5 A - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
05-Jan-1996
ACCESSIONS JC2132
REFERENCE #authors Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;
Sugiyama, H.
#journal Biochem. Biophys. Res. Commun. (1994) 199:1136-1143
#title Molecular cloning and the functional expression of two
isoforms of human metabotropic glutamate receptor subtype
5.
#cross-references MUID:94197696
#accession JC2132
#molecule_type mRNA
#residues 1-1180 #label MIN
COMMENT This protein is coupled to guanine nucleotide binding proteins.
KEYWORDS glycoprotein; neurotransmitter; receptor; transmembrane
protein
FEATURE
580-604 #domain transmembrane #status predicted #label TM1\
617-637 #domain transmembrane #status predicted #label TM2\
644-664 #domain transmembrane #status predicted #label TM3\
694-714 #domain transmembrane #status predicted #label TM4\
738-759 #domain transmembrane #status predicted #label TM5\
773-794 #domain transmembrane #status predicted #label TM6\
803-827 #domain transmembrane #status predicted #label TM7\
SUMMARY #length 1180 #molecular-weight 129053 #checksum 237

Query Match 3.3%; Score 215; DB 2; Length 1180;
Best Local Similarity 28.3%; Pred. No. 6.10e-14;
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;

Db 656 AMSYSALVTNRIARILAGSK-KKICTKPRFMSACA-OLVIAF-ILIC---IQ-LGII 708
QY 522 TTAFGAMFAKTRVHAIFKNVMKKIIKDQKLLYIVGGMLLIDICILICQWADVPLRT 581
Db 709 VALFIMEPDDIMHDYPSIREVYLICNTNLGV-VTPL-GYNGLLIL-SCTFYAFKTRNP 765
QY 582 VEKYSMEPDPAGRDI-SIRPLEHCENTHMTWILGIYVAYKGLMLFGC-FLAWETRNV 639
Db 766 -ANFNEAKVIAFTMTTCIILWAFVPI-YFGSNYKIITMCF-S-VSL-SATVALGCM-FV 819
QY 640 IPALNDSKYIGMSVYNGVIMCIIGAASVFLTRDQPNVQFCIIVALVIIFCSTITL-CLV 698
Db 820 PKVYIILAKPE 830
QY 699 PKLITLRTNPD 709

RESULT 9
ENTRY JC2131 #type complete
TITLE metabotropic glutamate receptor 5 B - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
05-Jan-1996

```



(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Mar 15 21:44:59 2000; MasPar time 14.45 Seconds

Tabular output not generated. 805.278 Million cell updates/sec

Title: >US-09-211-755-2
Description: (1-898) from US09211755.pep
Perfect Score: 6573
Sequence: 1 MPSCPARSATGPLSINGLMP.....TASPRHRHYPPSPRVMSGL 898

Scoring table: PAM 150
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 36.509; Variance 186.922; scale 0.195

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	225	3.4	877	2	US-08-407- Sequence 2, Applicatio	1.59e-07
2	225	3.4	912	3	PCT-US91-0 Sequence 19, Applicati	1.59e-07
3	214	3.3	915	1	US-08-453- Sequence 2, Applicati	1.01e-06
4	214	3.3	915	2	US-08-452- Sequence 2, Applicati	1.01e-06
5	214	3.3	915	3	PCT-US94-1 Sequence 2, Applicati	1.01e-06
6	189	2.9	905	1	US-08-072- Sequence 2, Applicati	6.38e-05
7	189	2.9	1079	1	US-08-485- Sequence 8, Applicati	6.38e-05
8	189	2.9	1079	2	US-08-943- Sequence 8, Applicati	6.38e-05
9	189	2.9	1079	1	US-08-484- Sequence 8, Applicati	6.38e-05
10	189	2.9	1079	2	US-08-480- Sequence 8, Applicati	6.38e-05
11	188	2.9	1180	1	US-08-072- Sequence 8, Applicati	7.51e-05
12	188	2.9	1212	1	US-08-072- Sequence 10, Applicati	7.51e-05
13	181	2.8	877	1	US-08-072- Sequence 12, Applicati	2.35e-04
14	187	2.8	879	1	US-08-072- Sequence 6, Applicati	8.85e-05
15	187	2.8	879	1	US-08-486- Sequence 2, Applicati	1.04e-04
16	186	2.8	906	1	US-08-486- Sequence 2, Applicati	1.04e-04
17	186	2.8	906	3	PCT-US91-0 Sequence 17, Applicati	1.04e-04
18	186	2.8	1056	2	US-08-687- Sequence 7, Applicati	1.04e-04
19	186	2.8	1056	2	US-08-687- Sequence 8, Applicati	1.04e-04
20	186	2.8	1058	2	US-08-687- Sequence 5, Applicati	1.04e-04
21	184	2.8	1078	2	US-08-943- Sequence 7, Applicati	1.44e-04
22	184	2.8	1078	1	US-08-485- Sequence 7, Applicati	1.44e-04
23	184	2.8	1078	2	US-08-480- Sequence 7, Applicati	1.44e-04

24	184	2.8	1078	1	US-08-484- Sequence 7, Applicatio	1.44e-04
25	182	2.8	1085	2	US-08-480- Sequence 5, Applicatio	2.00e-04
26	182	2.8	1085	1	US-08-484- Sequence 5, Applicatio	2.00e-04
27	182	2.8	1085	1	US-08-485- Sequence 5, Applicatio	2.00e-04
28	182	2.8	1085	2	US-08-943- Sequence 5, Applicatio	2.00e-04
29	184	2.8	1088	2	US-08-943- Sequence 6, Applicatio	1.44e-04
30	184	2.8	1088	2	US-08-480- Sequence 6, Applicatio	1.44e-04
31	184	2.8	1088	1	US-08-484- Sequence 6, Applicatio	1.44e-04
32	184	2.8	1088	1	US-08-485- Sequence 6, Applicatio	1.44e-04
33	184	2.8	1180	1	US-08-486- Sequence 8, Applicatio	1.44e-04
34	186	2.8	1199	1	US-08-463- Sequence 2, Applicatio	1.04e-04
35	186	2.8	1199	1	US-08-041- Sequence 2, Applicatio	1.04e-04
36	186	2.8	1199	2	US-08-465- Sequence 2, Applicatio	1.04e-04
37	186	2.8	1199	1	US-08-455- Sequence 2, Applicatio	1.04e-04
38	186	2.8	1199	3	PCT-US91-0 Sequence 2, Applicatio	1.04e-04
39	184	2.8	1212	1	US-08-486- Sequence 10, Applicati	1.44e-04
40	184	2.8	1219	2	US-08-687- Sequence 6, Applicatio	1.44e-04
41	177	2.7	877	1	US-08-486- Sequence 12, Applicati	4.50e-04
42	127	1.9	922	2	US-08-486- Sequence 20, Applicati	1.11e+00
43	127	1.9	922	2	US-08-231- Sequence 14, Applicati	1.11e+00
44	127	1.9	976	2	US-08-231- Sequence 22, Applicati	1.11e+00
45	127	1.9	976	2	US-08-486- Sequence 22, Applicati	1.11e+00

ALIGNMENTS

RESULT 1
ID US-08-407-875-2 STANDARD; PRT; 877 AA.
XX xxxxxx
XX
DT
XX
DE Sequence 2, Application US/08407875
XX
CC Sequence 2, Application US/08407875
CC Patent No. 5912122
CC GENERAL INFORMATION:
CC APPLICANT: Dagget, Lorrie
CC APPLICANT: Lu, Chin-Chun
CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
CC TITLE OF INVENTION: SUBTYPE mGluR6, NUCLEIC ACIDS ENCODING SAME AND USES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
CC STREET: 444 South Flower Street, Suite 2000
CC CITY: Los Angeles
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/407,875
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Reiter, Stephen E.
CC REGISTRATION NUMBER: 31,192
CC REFERENCE/DOCKET NUMBER: P41 9921
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-546-4737
CC TELEFAX: 619-546-9392
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 877 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein

SQ SEQUENCE 877 AA; 95436 MW; 4127619 CN;

Query Match 3.4%; Score 225; DB 2; Length 877;
Best Local Similarity 21.5%; Pred. No. 1.59e-07;
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

Db 592 LAVLGIVATTVAIVFVRYNNTPIVRASGRLSYVLLTGIFLIYA-I-TF-L---MVAEP 645
QY 445 LTILGIMASAFLEFFNKNRQKLIKMSPPYNNLIILGGLMSYASIFLGLDGSFVSEK 504

Db 646 G-AAYCAARLEFLGSLTSLTSALITKRIYRIFEOGKRSVTPPPFISPTSLQVITFSL 704
QY 505 TFEELCTVETWLTIVGYITAFGAMFAKTRVHAIFKNVK--MKKK-IKQKQLLVIVGGM 561

Db 705 TSLQVGMTANLARGPPHSVID-YE-EQRTVDPEQA-RGVLK-CDMSDLSL-TGCL-GY-757
QY 562 LLDLDGILICWQAVDPLRRTVEKYSMEPDAGRDISIRPLEHCENTHMTIWIIGIVAYK 621

Db 758 SLILMVTC-TVYAIKARGVPETFEAKPIGTMTYTCIILWLAFAPIFGTAQSAEKIYIQ 816
QY 622 GLLMLFGCFLANETRNVSIP-ALNDSKYIGMSVYNNVGMICLIIGAASVFLTDQPNVQFC-679

Db 817 TTTLVSLSLASVSIGMLYVPKTVIILFHPQNVQKRR 855
QY 680 IVALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNR 716

RESULT 2
ID PCT-US91-09422-19 STANDARD; PRT; 912 AA.
XX
AC xxxxxx

Sequence 19, Application PC/TUS9109422

Sequence 19, Application PC/TUS9109422
GENERAL INFORMATION:
APPLICANT: Mulvihill, Eileen R.
APPLICANT: Hagen, Frederick S.
APPLICANT: Houamed, Khaled M.
APPLICANT: Almers, Wolfhard
TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94103-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09422
FILING DATE: 19911212
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,007
FILING DATE: 18-MAR-1991
APPLICATION NUMBER: US 07/648,481
FILING DATE: 30-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,806
FILING DATE: 12-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-6PC

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 467-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 912 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 912 AA; 102014 MW; 4464621 CN;

Query Match 3.4%; Score 225; DB 3; Length 912;
Best Local Similarity 22.6%; Pred. No. 1.59e-07;
Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

Db 598 AVLPFLFVAVG-IAATLFFVVTFRNDPIVRASGRLSYVLLAGIFLCYATTEL--M-643
QY 440 SILSA-LTILGIMASAFLEFFN-IKNRQKLIKMSPPYNNLIILGGLMSYASIFLGLD 497

Db 644 --TAEPLDGT-CSLRRIFLGLGMSISYAALLPKTKRIYRIFEOGKRSVAPRFISPASQ 699
QY 498 GSFVSEKTFELCTVETWLTIVGYITAFGAMFAKTRVHAIFKNVK--MKK-KIKDQKL 554

Db 700 LAIT--FILISLQLLGICVWVVDPSHSVVD-FDQRTLDPR-FA-RGVLK-CDISDLSL 753
QY 555 LVIVGGMLLIDLCL-IC-WQAVDPLRRTVEKYSMEPDAGRDISIRPLEHCENTHMTI 612

Db 754 -ICLL-GYSMLLV-TC-TVYAIKTRGVPEFNEAKPIGTMTYTCIIVLAIFPIFFGTS 809
QY 613 WLGIVYAYKGLLMLFGCFLANETRNVSIP-ALNDSKYIGMSVYNNVGMICLIIGAASVFLTR 671

Db 810 QSADKLXIQTTLTVSVSLASVSIGMLYMPKYIILFHPQNVQKRR 857
QY 672 DQPNVQFC-I VALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNR 716

RESULT 3
ID US-08-453-862-2 STANDARD; PRT; 915 AA.
XX
AC xxxxxx

Sequence 2, Application US/08453862

Sequence 2, Application US/08453862
Patent No. 5738999
GENERAL INFORMATION:
APPLICANT: Segerson, Thomas P.
APPLICANT: Kinzie, J. Mark
APPLICANT: Mulvihill, Eileen R.
APPLICANT: Saugstad, Julie A.
APPLICANT: Westbrook, Gary L.
TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,862
FILING DATE: 30-MAY-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,401

CC FILING DATE: 30-DEC-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Parmelee, Steven W.
CC REGISTRATION NUMBER: 31,990
CC REFERENCE/DOCKET NUMBER: 13952-18-2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-467-9600
CC TELEFAX: 415-576-0300
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 915 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;
Query Match 3.3%; Score 214; DB 1; Length 915;
Best Local Similarity 22.9%; Pred. No. 1.01e-06;
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;
Db 597 LAMLGII-ATIFVMAFIRYNDTPIVRASGRELVSLLTGIFLCY--IITF-L---MIA- 648
QY 445 LTIILGIMASAFLEFN--IKNRNQLIKMSSPYMNNLIILGMLSYASIFLFGDGSFVSE 503
Db 649 KPDVAVCSFRRVFLGLGMCISYAALLTKNRIYRIFEOGKKSVTAPRLISPTSQLAITSS 708
QY 504 KTFEILCTVTRTWLVVGYTTAFGAMFAKTRVHAIFKNVEMK-K--KIIDQKLLVIVGG 560
Db 709 LISVOLLGVFI-WFGVDPPNIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761
QY 561 MLLIDL-CILICQAVDPLRTVEKYSMEPPAGRDISRPLEHCENTHMTIWLGIYVA 619
Db 762 YSILLMV-TC-TVYAIKTRGVPENFENAKPIGFTMYTTCIVWLAFIPFGTAQSAEKLY 819
QY 620 YKGLMLFCFLAWETRNVSIPA-LNDSKYLGMVYVNGIMCIIGAASVFLTRDQPNVOF 678
Db 820 IQTTLTISMNLSASVALGMLYMPKVIYIIIFHPELNVOKRRSF 863
QY 679 C-IVALVI-I-FCSTITLCVFPVKLIITLRNPDAATQNRROF 719
RESULT 4
ID US-08-452-734A-2 STANDARD; PRT; 915 AA.
XX
AC xxxxxx
DT
DE
XX Sequence 2, Application US/08452734A
CC Sequence 2, Application US/08452734A
CC Patent No. 5831047
CC GENERAL INFORMATION:
CC APPLICANT: Segerson, Thomas P.
CC APPLICANT: Kinzie, J. Mark
CC APPLICANT: Mulvihill, Eileen R.
CC APPLICANT: Saugstad, Julie A.
CC APPLICANT: Westbrook, Gary L.
CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC PRIOR APPLICATION NUMBER: US 08/176,401
CC FILING DATE: 30-DEC-1993
CC ATTORNEY/AGENT INFORMATION:

CC APPLICATION NUMBER: US/08/452,734A
CC FILING DATE: 30-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/176,401
CC FILING DATE: 30-DEC-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Parmelee, Steven W.
CC REGISTRATION NUMBER: 31,990
CC REFERENCE/DOCKET NUMBER: 13952-18-1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-467-9600
CC TELEFAX: 415-576-0300
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 915 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;
Query Match 3.3%; Score 214; DB 2; Length 915;
Best Local Similarity 22.9%; Pred. No. 1.01e-06;
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;
Db 597 LAMLGII-ATIFVMAFIRYNDTPIVRASGRELVSLLTGIFLCY--IITF-L---MIA- 648
QY 445 LTIILGIMASAFLEFN--IKNRNQLIKMSSPYMNNLIILGMLSYASIFLFGDGSFVSE 503
Db 649 KPDVAVCSFRRVFLGLGMCISYAALLTKNRIYRIFEOGKKSVTAPRLISPTSQLAITSS 708
QY 504 KTFEILCTVTRTWLVVGYTTAFGAMFAKTRVHAIFKNVEMK-K--KIIDQKLLVIVGG 560
Db 709 LISVOLLGVFI-WFGVDPPNIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761
QY 561 MLLIDL-CILICQAVDPLRTVEKYSMEPPAGRDISRPLEHCENTHMTIWLGIYVA 619
Db 762 YSILLMV-TC-TVYAIKTRGVPENFENAKPIGFTMYTTCIVWLAFIPFGTAQSAEKLY 819
QY 620 YKGLMLFCFLAWETRNVSIPA-LNDSKYLGMVYVNGIMCIIGAASVFLTRDQPNVOF 678
Db 820 IQTTLTISMNLSASVALGMLYMPKVIYIIIFHPELNVOKRRSF 863
QY 679 C-IVALVI-I-FCSTITLCVFPVKLIITLRNPDAATQNRROF 719
RESULT 5
ID PCT-US94-14989-2 STANDARD; PRT; 915 AA.
XX
AC xxxxxx
DT
DE
XX Sequence 2, Application PC/TUS9414989
CC Sequence 2, Application PC/TUS9414989
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
CC NUMBER OF SEQUENCES: 3
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/14989
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/176,401
CC FILING DATE: 30-DEC-1993
CC ATTORNEY/AGENT INFORMATION:

CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,565
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;
CC
CC Query Match 2.9%; Score 189; DB 1; Length 1079;
CC Best Local Similarity 27.5%; Pred. No. 6.38e-05;
CC Matches 25; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
CC
Db 125 LDECNCSSEHTPTSIYVVGATGSGVTANLLGLFYIPQVSYASSRLLSNKNQYKSF 184
QY 71 LKAFYDAIKYGNHLMVFGVCPSTVSIIAESLQGNLNLVQLSFAATTPVLADKKRYPYFF 130
Db 185 FTIPNDEHQATMADIIEYFRWNVGTIAAD 215
QY 131 RTVPSDNVAVNPAIKLKLKHYQWRKRGVTLTQD 161
CC
CC RESULT 10
CC ID US-08-480-751-8 STANDARD; PRT; 1079 AA.
CC XX
CC AC xxxxxx

Sequence 8, Application US/08480751
Sequence 8, Application US/08480751
Patent No. 5858684
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 1079 AA; 120867 MW; 6054255 CN;
Query Match 2.9%; Score 189; DB 2; Length 1079;
Best Local Similarity 27.5%; Pred. No. 6.38e-05;
Matches 25; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
Query Match 2.9%; Score 189; DB 2; Length 1079;
Best Local Similarity 27.5%; Pred. No. 6.38e-05;